```
   1 TCCTCCGGTC GCCCGCCCTC GGGGCAGCTA GTGGCGCAGC CCCCCGCCCG
  51 CGGCCCTGGC CTCCCGGGCG GCGCGGCAGG GGAGGGGTTA AGCTGCCGCA
 101 GGGACCGCCG CGTGCGGGGC GAGAGGGAGC CCCCGGTGGG GGTGGCGCAG
 151 CCGGCGGGGT TCGGTCCGAG CCCGGTGGGA GGCTCCCGGA GCGCAGCCTG
 201 GGCCCAGCCC ACCCCGCGCC GGCGGCCATG GCAGGCACCC TGGACCTGGA
 251 CAAGGGCTGC ACGGTGGAGG AGCTGCTCCG CGGGTGCATC GAAGCCTTCG
 301 ATGACTCCGG GAAGGTGCGG GACCCGCAGC TGGTGCGCAT ATTCCTCATG
 351 ATGCACCCCT GGTACATCCC CTCCTCTCAG CTGGCGGCCA AGCTGCTCCA
 401 CATCTACCAA CAATCCCGGA AGGACAACTC CAATTCCCTG CAGGTGAAAA
 451 CGTGCCACCT GGTCAGGTAC TGGATCTCCG CCTTCCCAGC GGAGTTTGAC
 501 TTGAACCCGG AGTTGGCTGA GCAGATCAAG GAGCTGAAGG CTCTGCTAGA
 551 CCAAGAAGGG AACCGACGGC ACAGCAGCCT AATCGACATA GACAGCGTCC
 601 CTACCTACAA GTGGAAGCGG CAGGTGACTC AGCGGAACCC TGTGGGACAG
 651 AAAAAGCGCA AGATGTCCCT GTTGTTTGAC CACCTGGAGC CCATGGAGCT
 701 GGCGGAGCAT CTCACCTACT TGGAGTATCG CTCCTTCTGC AAGATCCTGT
 751 TTCAGGACTA TCACAGTTTC GTGACTCATG GCTGCACTGT GGACAACCCC
 801 GTCCTGGAGC GGTTCATCTC CCTCTTCAAC AGCGTCTCAC AGTGGGTGCA
 851 GCTCATGATC CTCAGCAAAC CCACAGCCCC GCAGCGGGCC CTGGTCATCA
 901 CACACTTTGT CCACGTGGCG GAGAAGCTGC TACAGCTGCA GAACTTCAAC
 951 ACGCTGATGG CAGTGGTCGG GGGCCTGAGC CACAGCTCCA TCTCCCGCCT
1001 CAAGGAGACC CACAGCCACG TTAGCCCTGA GACCATCAAG CTCTGGGAGG
1051 GTCTCACGGA ACTAGTGACG GCGACAGGCA ACTATGGCAA CTACCGGCGT
1101 CGGCTGGCAG CCTGTGTGGG CTTCCGCTTC CCGATCCTGG GTGTGCACCT
1151 CAAGGACCTG GTGGCCCTGC AGCTGGCACT GCCTGACTGG CTGGACCCAG
1201 CCCGGACCCG GCTCAACGGG GCCAAGATGA AGCAGCTCTT TAGCATCCTG
1251 GAGGAGCTGG CCATGGTGAC CAGCCTGCGG CCACCAGTAC AGGCCAACCC
1301 CGACCTGCTG AGCCTGCTCA CGGTGTCTCT GGATCAGTAT CAGACGGAGG
1351 ATGAGCTGTA CCAGCTGTCC CTGCAGCGGG AGCCGCGCTC CAAGTCCTCG
1401 CCAACCAGCC CCACGAGTTG CACCCCACCA CCCCGGCCCC CGGTACTGGA
1451 GGAGTGGACC TCGGCTGCCA AACCCAAGCT GGATCAGGCC CTCGTGGTGG
1501 AGCACATCGA GAAGATGGTG GAGTCTGTGT TCCGGAACTT TGACGTCGAT
1551 GGGGATGGCC ACATCTCACA GGAAGAATTC CAGATCATCC GTGGGAACTT
1601 CCCTTACCTC AGCGCCTTTG GGGACCTCGA CCAGAACCAG GATGGCTGCA
1651 TCAGCAGGGA GGAGATGGTT TCCTATTTCC TGCGCTCCAG CTCTGTGTTG
1701 GGGGGGCGCA TGGGCTTCGT ACACAACTTC CAGGAGAGCA ACTCCTTGCG
1751 CCCCGTCGCC TGCCGCCACT GCAAAGCCCT GATCCTGGGC ATCTACAAGC
1801 AGGGCCTCAA ATGCCGAGCC TGTGGAGTGA ACTGCCACAA GCAGTGCAAG
1851 GATCGCCTGT CAGTTGAGTG TCGGCGCAGG GCCCAGAGTG TGAGCCTGGA
1901 GGGGTCTGCA CCCTCACCCT CACCCATGCA CAGCCACCAT CACCGCGCCT
1951 TCAGCTTCTC TCTGCCCCGC CCTGGCAGGC GAGGCTCCAG GCCTCCAGCA
2001 ATCCCCCTCC CAGCAGAGAT CCGTGAGGAG GAGGTACAGA CGGTGGAGGA
2051 TGGGGTGTTT GACATCCACT TGTAATAGAT GCTGTGGTTG GATCAAGGAC
2101 TCATTCCTGC CTTGGAGAAA ATACTTCAAC CAGAGCAGGG AGCCTGGGGG
2151 TGTCGGGGCA GGAGGCTGGG GATGGGGGTG GGATATGAGG GTGGCATGCA
2201 GCTGAGGGCA GGGCCAGGGC TGGTGTCCCT AAGGTTGTAC AGACTCTTGT
2251 GAATATTTGT ATTTTCCAGA TGGAATAAAA AGGCCCGTGT AATTAAAAAA
2301 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA  (SEQ ID NO:1)
```

FEATURES:
```
5'UTR:        1-227
Start Codon: 228
Stop Codon:  2073
3'UTR:        2076
```

FIGURE 1A

Homologous proteins:
Top 10 BLAST Hits

	Score	E
CRA|1000682340958 /altid=gi|6358505 /def=gb|AAF07219.1|AF043722...	1293	0.0
CRA|18000005086608 /altid=gi|5031623 /def=ref|NP_005816.1| RAS ...	1241	0.0
CRA|18000005188697 /altid=gi|6755290 /def=ref|NP_035372.1| RAS,...	1202	0.0
CRA|18000005205935 /altid=gi|7662334 /def=ref|NP_056191.1| KIAA...	618	e-175
CRA|18000005188699 /altid=gi|3928857 /def=gb|AAC79700.1| (AF081...	533	e-150
CRA|18000005152782 /altid=gi|9507035 /def=ref|NP_062084.1| RAS ...	531	e-149
CRA|18000005192860 /altid=gi|7242201 /def=ref|NP_035376.1| RAS ...	529	e-149
CRA|18000005192861 /altid=gi|4038292 /def=gb|AAC97349.1| (AF106...	526	e-148
CRA|18000005188698 /altid=gi|5032025 /def=ref|NP_005730.1| RAS ...	525	e-148
CRA|1000733831533 /altid=gi|6650545 /def=gb|AAF21898.1|AF081197...	525	e-148

BLAST dbEST hits:

	Score	E
gi|5432583 /dataset=dbest /taxon=9606 ...	1310	0.0
gi|9876673 /dataset=dbest /taxon=960...	1281	0.0
gi|11286864 /dataset=dbest /taxon=96...	1249	0.0
gi|11285315 /dataset=dbest /taxon=96...	1207	0.0
gi|5432584 /dataset=dbest /taxon=9606 ...	733	0.0
gi|4372300 /dataset=dbest /taxon=9606 ...	720	0.0
gi|12295751 /dataset=dbest /taxon=96...	700	0.0
gi|12288965 /dataset=dbest /taxon=96...	599	e-168
gi|6920402 /dataset=dbest /taxon=960...	573	e-161
gi|2005039 /dataset=dbest /taxon=9606 ...	573	e-161

EXPRESSION INFORMATION FOR MODULATORY USE:
library source:
From BLAST dbEST hits:
gi\|5432583 Testis
gi\|9876673 Liver-non-cancerous
gi\|11286864 Brain glioblastoma
gi\|11285315 Brain glioblastoma
gi\|5432584 Testis
gi\|4372300 B Cell Chronic lymphatic leukemia
gi\|12295751 Adult marrow
gi\|12288965 Adult marrow
gi\|6920402 Lymph germinal center B cell
gi\|2005039 Lymph

From tissue screening panels:
Leukocyte

FIGURE 1B

```
  1 MAGTLDLDKG CTVEELLRGC IEAFDDSGKV RDPQLVRIFL MMHPWYIPSS
 51 QLAAKLLHIY QQSRKDNSNS LQVKTCHLVR YWISAFPAEF DLNPELAEQI
101 KELKALLDQE GNRRHSSLID IDSVPTYKWK RQVTQRNPVG QKKRKMSLLF
151 DHLEPMELAE HLTYLEYRSF CKILFQDYHS FVTHGCTVDN PVLERFISLF
201 NSVSQWVQLM ILSKPTAPQR ALVITHFVHV AEKLLQLQNF NTLMAVVGGL
251 SHSSISRLKE THSHVSPETI KLWEGLTELV TATGNYGNYR RRLAACVGFR
301 FPILGVHLKD LVALQLALPD WLDPARTRLN GAKMKQLFSI LEELAMVTSL
351 RPPVQANPDL LSLLTVSLDQ YQTEDELYQL SLQREPRSKS SPTSPTSCTP
401 PPRPPVLEEW TSAAKPKLDQ ALVVEHIEKM VESVFRNFDV DGDGHISQEE
451 FQIIRGNFPY LSAFGDLDQN QDGCISREEM VSYFLRSSSV LGGRMGFVHN
501 FQESNSLRPV ACRHCKALIL GIYKQGLKCR ACGVNCHKQC KDRLSVECRR
551 RAQSVSLEGS APSPSPMHSH HHRAFSFSLP RPGRRGSRPP AIPLPAEIRE
601 EEVQTVEDGV FDIHL  (SEQ ID NO:2)
```

FEATURES:
Functional domains and key regions:
[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3
```
      1   113-116 RRHS
      2   144-147 RKMS
      3   584-587 RRGS
```

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7
```
      1    27-29 SGK
      2    63-65 SRK
      3   126-128 TYK
      4   134-136 TQR
      5   269-271 TIK
      6   349-351 SLR
      7   506-508 SLR
```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 9
```
      1    12-15 TVEE
      2    63-66 SRKD
      3   117-120 SLID
      4   163-166 TYLE
      5   339-342 SILE
      6   373-376 TEDE
      7   447-450 SQEE
      8   476-479 SREE
      9   605-608 TVED
```

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 4
```
      1    19-24 GCIEAF
      2   249-254 GLSHSS
      3   284-289 GNYGNY
      4   492-497 GGRMGF
```

FIGURE 2A

[5] PDOC00009 PS00009 AMIDATION
Amidation site

      582-585 PGRR

[6] PDOC00018 PS00018 EF_HAND
EF-hand calcium-binding domain

Number of matches: 2
      1   439-451 DVDGDGHISQEEF
      2   468-480 DQNQDGCISREEM

[7] PDOC00379 PS00479 DAG_PE_BIND_DOM_1
Phorbol esters / diacylglycerol binding domain

      499-548 HNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLSVEC

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	34	54	0.713	Putative
2	195	215	0.653	Putative
3	238	258	0.788	Putative

FIGURE 2B

BLAST Alignment to Top Hit:

```
>CRA|18000005086608 /altid=gi|5031623 /def=ref|NP_005816.1| RAS guanyl
            releasing protein 2 (calcium and DAG-regulated); calcium
            and diacylglycerol-regulated guanine nucleotide exchange
            factor I [Homo sapiens] /org=Homo sapiens /taxon=9606
            /dataset=nraa /length=609
          Length = 609
 Score = 1241 bits (3176), Expect = 0.0
 Identities = 608/615 (98%), Positives = 609/615 (98%)
 Frame = +3
```

```
Query: 228   MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 407
             MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY
Sbjct: 1     MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60


Query: 408   QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 587
             QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID
Sbjct: 61    QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120


Query: 588   IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 767
             IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
Sbjct: 121   IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180


Query: 768   FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 947
             FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF
Sbjct: 181   FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240


Query: 948   NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 1127
             NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR
Sbjct: 241   NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300


Query: 1128  FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 1307
             FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL
Sbjct: 301   FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360


Query: 1308  LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 1487
             LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ
Sbjct: 361   LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420


Query: 1488  ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 1667
             ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM
Sbjct: 421   ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480


Query: 1668  VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847
             VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
Sbjct: 481   VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540


Query: 1848  KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 2027
             KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP      EIRE
Sbjct: 541   KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP------EIRE 594


Query: 2028  EEVQTVEDGVFDIHL 2072
             EEVQTVEDGVFDIHL
Sbjct: 595   EEVQTVEDGVFDIHL 609    (SEQ ID NO:4)
```

FIGURE 2C

```
>CRA|1000682340958 /altid=gi|6358505 /def=gb|AAF07219.1|AF043722_1
          (AF043722) guanine exchange factor MCG7 isoform 1 [Homo
          sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
          /length=671
          Length = 671
 Score = 1293 bits (3309), Expect = 0.0
 Identities = 639/670 (95%), Positives = 643/670 (95%), Gaps = 4/670 (0%)
 Frame = +3


Query: 75    GRGGVKLPQGPPRAGREGAPGGGGAAG----GVRSEPGGRLPERSLGPAHPAPAAMAGTL 242
             GRG   P   +  +E    G   +G      GVRSEPGGRLPERSLGPAHPAPAAMAGTL
Sbjct: 8     GRGTQGWPGSSEQHVQEATSSAGLHSGVDELGVRSEPGGRLPERSLGPAHPAPAAMAGTL 67


Query: 243   DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIYQQSRK 422
             DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIYQQSRK
Sbjct: 68    DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIYQQSRK 127


Query: 423   DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP 602
             DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP
Sbjct: 128   DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP 187


Query: 603   TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG 782
             TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG
Sbjct: 188   TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG 247


Query: 783   CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA 962
             CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA
Sbjct: 248   CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA 307


Query: 963   VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG 1142
             VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG
Sbjct: 308   VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG 367


Query: 1143  VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT 1322
             VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT
Sbjct: 368   VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT 427


Query: 1323  VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE 1502
             VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE
Sbjct: 428   VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE 487


Query: 1503  HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL 1682
             HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL
Sbjct: 488   HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL 547


Query: 1683  RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS 1862
             RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS
Sbjct: 548   RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS 607


Query: 1863  VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIREEEVQT 2042
             VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP      EIREEEVQT
Sbjct: 608   VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP------EIREEEVQT 661


Query: 2043  VEDGVFDIHL 2072
             VEDGVFDIHL
Sbjct: 662   VEDGVFDIHL 671   (SEQ ID NO:5)
```

FIGURE 2D

```
>CRA|18000005188697 /altid=gi|6755290 /def=ref|NP_035372.1| RAS,
          guanyl releasing protein 2; RAP 1A protein-specific
          guanine nucleotide exchange factor 1; CalDAG-GEFI [Mus
          musculus] /org=Mus musculus /taxon=10090 /dataset=nraa
          /length=608
          Length = 608
 Score = 1202 bits (3076), Expect = 0.0
 Identities = 589/615 (95%), Positives = 597/615 (96%)
 Frame = +3


Query: 228  MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 407
            MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y
Sbjct: 1    MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLHFY 60


Query: 408  QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 587
            QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNPELAE IKELKALLDQEGNRRHSSLID
Sbjct: 61   QQSRKDNSNSLQVKTCHLVRYWVSAFPAEFDLNPELAEPIKELKALLDQEGNRRHSSLID 120


Query: 588  IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 767
            I+SVPTYKWKRQVTQRNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
Sbjct: 121  IESVPTYKWKRQVTQRNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180


Query: 768  FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 947
            FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA QRALVITHFVHVAEKLLQLQNF
Sbjct: 181  FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQRALVITHFVHVAEKLLQLQNF 240


Query: 948  NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 1127
            NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR
Sbjct: 241  NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300


Query: 1128 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 1307
            FPILGVHLKDLVALQLALPDWLDP RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL
Sbjct: 301  FPILGVHLKDLVALQLALPDWLDPGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360


Query: 1308 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 1487
            LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTS AKPKLDQ
Sbjct: 361  LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSVAKPKLDQ 420


Query: 1488 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 1667
            ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM
Sbjct: 421  ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480


Query: 1668 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847
            +SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
Sbjct: 481  ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540


Query: 1848 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 2027
            KDRLSVECRRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP      EIRE
Sbjct: 541  KDRLSVECRRRAQSVSLEGSAPSPSPTHT-HHRAFSFSLPRPGRRSSRPP------EIRE 593


Query: 2028 EEVQTVEDGVFDIHL 2072
            EEVQTVEDGVFDIHL
Sbjct: 594  EEVQTVEDGVFDIHL 608   (SEQ ID NO:6)
```

FIGURE 2E

```
>CRA|18000005205935 /altid=gi|7662334 /def=ref|NP_056191.1| KIAA0846
          protein [Homo sapiens] /org=Homo sapiens /taxon=9606
          /dataset=nraa /length=689
        Length = 689
 Score =  618 bits (1576), Expect = e-175
 Identities = 314/597 (52%), Positives = 409/597 (67%), Gaps = 5/597 (0%)
 Frame = +3


Query: 234  GTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIYQQ 413
            G+  L K  T++ELL  CIE FDD+G++ +   L RI L+MH WY+ S++LA KLL +Y+
Sbjct: 2    GSSGLGKAATLDELLCTCIEMFDDNGELDNSYLPRIVLLMHRWYLSSTELAEKLLCMYRN 61


Query: 414  SRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDID 593
            +  ++ N  ++K C+ +RYWI  FPAEF+L+  L   +E + +  Q G  +H SLIDI
Sbjct: 62   ATGESCNEFRLKICYFMRYWILKFPAEFNLDLGLIRMTEEFREVASQLGYEKHVSLIDIS 121


Query: 594  SVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFV 773
            S+P+Y W R+VTQR  V  KK K  LLFDHLEP+ELAEHLT+LE++SF +I F DY S+V
Sbjct: 122  SIPSYDWMRRVTQRKKVS-KKGKACLLFDHLEPIELAEHLTFLEHKSFRRISFTDYQSYV 180


Query: 774  THGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNT 953
             HGC  +NP LER I+LFN +S+WVQLM+LSKPT  QRA VIT F++VA+KLLQL+NFNT
Sbjct: 181  IHGCLENNPTLERSIALFNGISKWVQLMVLSKPTPQQRAEVITKFINVAKKLLQLKNFNT 240


Query: 954  LMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFP 1133
            LMAVVGGLSHSSISRLKETHSH+S E  K W +TELV++ GNY NYR+  A C GF+ P
Sbjct: 241  LMAVVGGLSHSSISRLKETHSHLSSEVTKNWNEMTELVSSNGNYCNYRKAFADCDGFKIP 300


Query: 1134 ILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLS 1313
            ILGVHLKDL+A+ +  PDW +   ++N KM QL  L EL + +   ++ N DL++
Sbjct: 301  ILGVHLKDLIAVHVIFPDWTE--ENKVNIVKMHQLSVTLSELVSLQNASHHLEPNMDLIN 358


Query: 1314 LLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQAL 1493
            LLT+SLD Y TED++Y+LSL  EPR+  SPTSPT+     P +P V  EW      PK D +
Sbjct: 359  LLTLSLDLYHTEDDIYKLSLVLEPRNSKSPTSPTT---PNKPVVPLEWALGVMPKPDPTV 415


Query: 1494 VVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVS 1673
            + +HI K+VESVFRN+D D DG+ISQE+F+ I  NFP+L +F LD++QDG IS++EM++
Sbjct: 416  INKHIRKLVESVFRNYDHDHDGYISQEDFESIAANFPFLDSFCVLDKDQDGLISKDEMMA 475


Query: 1674 YFLRSSSVLGGRM--GFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847
            YFLR+ S L  +M  GF+HNFQE   L+P  C HC   + GI KQG KC+ CG NCHKQC
Sbjct: 476  YFLRAKSQLHCKMGPGFIHNFQEMTYLKPTFCEHCAGFLWGIIKQGYKCKDCGANCHKQC 535


Query: 1848 KDRLSVECRRRAQSVSL---EGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPL 2009
            KD L + CRR A++ SL   GS P  +     F F   G R    AI L
Sbjct: 536  KDLLVLACRRFARAPSLSSGHGSLPGSPSLPPAQDEVFEFPGVTAGHRDLDSRAITL 592    (SEQ
ID NO:7)


>CRA|18000005188699 /altid=gi|3928857 /def=gb|AAC79700.1|  (AF081196)
```

FIGURE 2F

```
           calcium and DAG-regulated guanine nucleotide exchange
           factor II [Rattus norvegicus] /org=Rattus norvegicus
           /taxon=10116 /dataset=nraa /length=795
              Length = 795
     Score =  533 bits (1358), Expect = e-150
     Identities = 267/590 (45%), Positives = 390/590 (65%), Gaps = 12/590 (2%)
     Frame = +3


Query: 156   GVRSEPGGRLPERSLGPAHPAPAAMAGTLD--------LDKGCTVEELLRGCIEAFDDS 308
             G R+ P GRL +S     PA  ++A           L KG ++++L+  CI++FD
Sbjct: 17    GSRAGPKGRLEAKSTNSPLPAQPSLAQITQFRMMVSLGHLAKGASLDDLIDSCIQSFDAD 76


Query: 309   GKV-RDPQLVRIFLMMHPWYIPSSQLAAKLLHIYQQSRKDNSNSLQVKTCHLVRYWISAF 485
             G + R  QL+++ L MH   I S++L   KL++++Y+ + + NS  + +K C+ VRYWI+ F
Sbjct: 77    GNLCRSNQLLQVMLTMHRIIISSAELLQKLMNLYKDALEKNSPGICLKICYFVRYWITEF 136


Query: 486   PAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVPTYKWKRQVTQRNPVG-QKKRK 662
                 F ++ L  ++E + L+    G   H  LID   + +  W R++TQR        KKRK
Sbjct: 137   WIMFKMDASLTSTMEEFQDLVKANGEESHCHLIDTTQINSRDWSRKLTQRIKSNTSKKRK 196


Query: 663   MSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHGCTVDNPVLERFISLFNSVSQ 842
             +SLLFDHLEP  EL+EHLTYLE++SF +I F DY +++ + C  +NP +ER I+L N +SQ
Sbjct: 197   VSLLFDHLEPEELSEHLTYLEFKSFRRISFSDYQNYLVNSCVKENPTMERSIALCNGISQ 256


Query: 843   WVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMAVVGGLSHSSISRLKETHSHV 1022
             WVQLM+LS+PT   RA V   F+HVA+KL QLQNFNTLMAV+GGL HSSISRLKET SHV
Sbjct: 257   WVQLMVLSRPTPQLRAEVFIKFIHVAQKLHQLQNFNTLMAVIGGLCHSSISRLKETSSHV 316


Query: 1023  SPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILGVHLKDLVALQLALPDWLDPA 1202
              E  K+   +TEL+++  NY NYRR   C  F+ PILGVHLKDL++L  A+PD+L+
Sbjct: 317   PHEINKVLGEMTELLSSCRNYDNYRRAYGECTHFKIPILGVHLKDLISLYEAMPDYLEDG 376


Query: 1203  RTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLTVSLDQYQTEDELYQLSLQRE 1382
             ++N  K+  L++ + EL  +  + PP+ AN DL+ LLT+SLD Y TEDE+Y+LS  RE
Sbjct: 377   --KVNVQKLLALYNHINELVQLQDVAPPLDANKDLVHLLTLSLDLYYTEDEIYELSYARE 434


Query: 1383  PRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVEHIEKMVESVFRNFDVDGDGH 1562
             PR+  +P        P +PPV+ +W S   PK D   + +H+++MV+SVF+N+D+D DG+
Sbjct: 435   PRNHRAPP-----LTPSKPPVVVDWASGVSPKPDPKTISKHVQRMVDSVFKNYDLDQDGY 489


Query: 1563  ISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFLRSSSVLGG-RMGFVHNFQES 1739
             ISQEEF+ I +FP+ +F +D++++G ISR+E+ +YF+R+SS+      +GF HNFQE+
Sbjct: 490   ISQEEFEKIAASFPF--SFCVMDKDREGLISRDEITAYFMRASSIYSKLGLGFPHNFQET 547


Query: 1740  NSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLSVECRRRAQS 1889
             L+P C +C + G+ KQG +C+ CG+NCHKQCKD +  EC++R++S
Sbjct: 548   TYLKPTFCDNCAGFLWGVIKQGYRCKDCGMNCHKQCKDLVVFECKKRSKS 597   (SEQ ID
NO:8)
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00617	RasGEF domain	123.5	4e-33	1
PF00130	Phorbol esters/diacylglycerol binding domain	59.5	3.6e-14	1
PF00036	EF hand	21.8	0.00027	2
PF01237	Oxysterol-binding protein	3.5	4.2	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01237	1/1	249	272 ..	1	24 [.	3.5	4.2

FIGURE 2G

```
PF00617   1/1    148   336 ..      1   227 []    123.5    4e-33
PF00036   1/2    430   458 ..      1    29 []     17.4   0.0047
PF00036   2/2    463   482 ..      5    24 ..      6.7      4.9
PF00130   1/1    499   548 ..      1    51 []     59.5  3.6e-14
```

FIGURE 2H

```
   1 ACAGAAAGGT CCTGTTTCTA AGTCTTACAT TACCAAGACT GAGGTGCGGG
  51 GGCGGTCCTG GATCCCCGC CCCAAGGCTG GGAGGGGCAC GCCTCGGAAG
 101 GGAGGTTTGG GGTCGGTGGT TTCACAGTGA GTGTGTCTGA AGCCAAATGG
 151 TCGGAAACCG TTACCCGCTC TCCTAGGCCC GGCTAGTGGG GACCCCAACC
 201 GCCTGCGGCT GCCCCTCCCA AGTTCCTCCC TGTTGGCCAG GCATCCAGGT
 251 CTCCAGTCTC CGAGCTGCGG AGAACCCACC GCCACATGCG GCTGCCCCTT
 301 TCCATTCGAC CCTGTGGGGA GCCAGGCTTC CGGGGCCCCG TTCCTCCTGT
 351 GTGAACTGGG CCCCCCGCCC CCATTCCCAG ACATCAAGGC CGCGTCTCCA
 401 GATAGCCACG ATTTCATTCC TCGCTCCCCA CAGGTCCCTC TCCCCAAAAT
 451 ATTCCCATCT TGTCCTAGCC CATCCCCCAG ACTATCTCAA GGACCAGCTG
 501 TCCCCACGCC CCCGACCTCC ACTAGGCCTG TGCCACCCGC TGCCTGCAGG
 551 AAGACGCCCG GTCCCGGGCC GGGTTAGCCC CATGGGAACG GTTTGTCTCG
 601 AAAACAGGAA CCCGAGCTGG GGGCTGGGCG GGGCGCCCCT TCCCCACCGC
 651 AGTCCGCTTC CTGCCCCTCC CGGCTTCCTC CGCCCGACAC CCAGGCAGGG
 701 CGGGGGGCAC TGGGGCGTCC GCGGTTGGGG GAGGGGCTCT TCGTTTCGGT
 751 CCCCCCTCCC GCGTCCCGGG CGGCGGGGCC TCCGGTCGCC CGCCTCGGGG
 801 CAGCTAGTGG CGCAGCCCCC CGCCCGCGGC CCTGGCCTCC CGGGCGGCGC
 851 GGCAGGGGAG GGGTTAAGCT GCCGCAGGGA CCGCCGCGTG CGGGGCGAGA
 901 GGGAGCCCCC GGTGGGGGTG GCGCAGCCGG CGGTGCGGAG CTCCGCGCAG
 951 GGGCGGAGGG GGGAGGGGGC AGCCTGGCGC GGGGGCGGGG GCGGGGCGGC
1001 GGGGAGCGGG GCCGCGGCGT GGAGAGCGGG CGGGAGCCGC AGCCGCAGCG
1051 AGGCCGGCGG GCGGGAGCGC ACGGAGGTGG GGTCGGCCAG GCCGGTGCGG
1101 GCTCCTTGCG GCAGGTCCCA AGAGTGAGTG GGCGAGCGCG GGCGGGGCGC
1151 CAGGCGAAGG AGGGCGCGGC CCCCAGCGAC TCCCCCCCCG CCCAGGGCGG
1201 CGCGGGCGGG CTGGGGGCGG CGAGCGGGTG GGGAGTCTGC GGCCCGGGTC
1251 TGGGAGAGGG GGCAGCGGCC ACGAGAGCTA AGGCGCGCTG GATCCCCGGA
1301 GGGCGGAGGA CCTCCACGGT GCACCCAGCT TTTCCCAGCC ACCTTCCAGC
1351 GGGGCCCTCC CCCGCGTACC CCCATTTGGC AGATGAGAAA ATTGAGGCTC
1401 CCAGAGGCCA AGTGATTCTC AAGGTCACAC GAGGAAGCGG TAGAGCCAGG
1451 CGGGGACGGC TCTGGGTGGC TCTTAGGAAA AGTCCGCCTG AGAACTCCGT
1501 ACAGGAGCTC CCCTGTCCTC CAGCCTGGGG GAGTGAGTAT GTGTAGGGCC
1551 GGGGTACCTT TCCGTGGGGC AAGGCTCTGC CAAAATCTGG GAGTGAGGGG
1601 AGTCAGGGAG CTGGGGCCGC AGGGCGGGCC CTGCACCGCA AATGGGAGGG
1651 GGGCGACGGA ATGGGCGTGC GCACCCATGG GGGTGTGTGC ATGTGTGTGG
1701 GAGTGTACAT GCGTGGAGAG GCACTGCCTT GCGTGTGTGC ACACGTGTGA
1751 GGATGTCAGC GCCTGTGTGG CCGCGGGACT CAAGGCTGGC CTGGCTCAAG
1801 TGAACAGCAC GTCCAGGAGG CGACCTCGTC CGCGGGTTTG CATTCTGGGG
1851 TGGACGAGCT GGGTATGTGT GCCTGAGGGT TTCTTCGTGC AGGTGTGCAC
1901 AGGGTGTGGG TGCCATTGTG TGTGAGAGAC GGAGGATGGG GAGGCCGGTG
1951 CCTGTGGCCC GGTGCGTGTA AGTGCGGACG CCTGCACCTC CACTTAGGTC
2001 CCCGGCCTCC GACGACTAAC TTGGGTGTGG AGTGTTTGCC CCTGCCAGGG
2051 TGCGTATGAC CCCGCCAGTG ACCGGAGTTG CTAATGGTGT CATGCACCCA
2101 CCGGCCACCC TTGGCGCGAG CGCCCCCCTC TGGACACCCT GCTCCGTGCG
2151 CGCTCACAGT TCGCCTGTGC GGGGCCGGGG CCAGGGTCAG GAGCCGGGGA
2201 TAGGGAGGAA GAGGGCCTGT GGACAAGCTG AGCCGGGACC CCTGGGACCT
2251 TTGCGGAGGT GGCCTGGGAG CGCTCAGTTC CCAGGCTGAG GCTTCCCGCT
2301 GACGCCTCCT GGCCGCAGCG GGCTCCCCCC GCCCCAGGAA TGTTCCTCTC
2351 CCATCCAGTC CGCCTCCCCT AGGGCAGGCC CCCTGGGGGC TGCCGCAGCC
2401 CCGCCTCGCC TTCCTGGGCT CCCGGGAGGG GGCGAGGCGA GCAGGACGCC
2451 TGGGTTCTCT CCCCCCACCT CCCATACCAG GGAGAAATTC CTCCGAGGTC
2501 CCCTCAGGCT CTGGGTTCCC AAAATAACCC TGCGGGGGAA GGGAGGCTGT
2551 GGAGGGAGGG AAGCGGGAGG GGCGCAGAGC CGAGCTGCGG GGTGCTGCAG
2601 GTGCCTCTGG GGAGAGGGCG CGAGGAGAAG CGCCCTGCG GGGGGCTGGG
2651 CGCCAGCCAG TCCTGGGATC TTGGTTCGTC CCCATCCTCG TGAAGCCCCT
2701 CGGCCTTCCC GCGACTCCGA GGGTGGGCCG GAAGCCTCTC TGCGGGTCCG
2751 TTTCCCAACT GGCGGGTTGC ACCATCCCGG GCCAGACCGT TTAACCCCGG
```

FIGURE 3A

```
2801 GAGTGGCCGC GGGGGACAAC TCCGCCCCTG TCCAGCAGGG GGCGTGCCCG
2851 CCCCGCCCCG TTTCTGCCCG CGGGGCCGCT CCCCCGCCCG CGACTCCGCA
2901 GACTCCCGCT CTGCCTCTCC CGGGACAGGG GTTCGGTCCG AGCCCGGTGG
2951 GAGGCTCCCG GAGCGCAGCC TGGGCCCAGC CCACCCCGCG CCGGCGGCCA
3001 TGGCAGGCAC CCTGGACCTG GACAAGGGCT GCACGGTGGA GGAGCTGCTC
3051 CGCGGGTGCA TCGAAGCCTT CGGTGAGTGG CTCGGGAGGG CACACGGAGC
3101 CTGAGCCTAG CCCCGAGTCT GAGCCCGGGT CCCTGCCTCC CAGGCACAGT
3151 CCAGGGCACA GCCCTGACCC GGACCCACCC TGCTCCGCAG CGTGCAGTCT
3201 CTTTAACGAA AGCCTCCTCC GCAACGCAGG GCAGAGAGAT GCACGCCCTT
3251 CAGACAGATG AGGTTTCCCT TCTCTAGCCT TCCCCAGCGG CGGCGAAGGG
3301 AGGGCCGGGT CCCGGACTCT GACACTTGAG GGGCATTATC TGTCTCCCGG
3351 GGAATCCGGA GGAACTCGCT ATCTCCGGCC TGGGAGCTGT TTCCGGCTAA
3401 TGGGGGGCGG CTTATCTGGT GAAGGGGTGC CCCTTCCCCC CAAGCGCTCA
3451 GGAAATGACC TCTGGATTCT TGACCCCGGG GAACCCAGGC TCCTTCCGCC
3501 CCAGCTGGTT CCCCTCCGGA CGATGGGCGG CTCGGGCGCT CCCCTCCTCC
3551 AGTCCTCAGG GCGTGCCTAT CTCTCGCCCA CCACACCTTT CCTCTCTAAT
3601 TTGCCTCCTG CTCTCGGAGT CCTGGGCAAG CAGGAGGTGG GCGGGGTCGA
3651 GCGTGCACCC GAAGGACCGA TACCTGGCGG GTTGCGGGGT GAGGATGAGG
3701 CATGGTAGCT GCGGACCCAG CTCAGCCACC TGTCTTTGAC CCTTCGGAGT
3751 CAGATGACTC CGGGAAGGTG CGGGACCCGC AGCTGGTGCG CATGTTCCTC
3801 ATGATGCACC CCTGGTACAT CCCCTCCTCT CAGCTGGCGG CCAAGCTGCT
3851 CCACATATAT CCTTCGCCGG CCTTGCCAAG GCCCCGCCG TCGGAGCCCA
3901 TGCGCAGCCC CTCTGCCCAG CCCAGGTGCA GAATGAGCCT CGCTCCTAAG
3951 TATAGGCCAC TCCTTATCCC AGAGCTCAGG CGTCGTCCCA GCCTCCAACT
4001 AGGGCCTAGG CTCTGCCCCC TCCTTGCTCC TAGCGACTCG GTCCTGTCCC
4051 CAGGCTCTGT CCCCAGCCGA GGCCTTGCCC TCCTTCTCCC TAGAGTCTAG
4101 GGCCTGCCCC TGCTTCAGGC TTGGGTGCGC CCCGTGCATC TCTCTCTCCC
4151 AGAGCCCAGG CTTTGCTTTC AGCCTCCCTC AGCACCTAGT CCTCCACCCC
4201 CACCTCCAAC CCCTCCCAGA GCTCAAGCCT CACCCCCAGC ATCTCCGCAG
4251 AGCGCAAGCC CCATCCCTAG AACGTGTCTC CTAGAACCAG GCCCCGCCCC
4301 CAGCCTCCCT CCACGCAGGC CTCCCTTTCT AGAGTTAAGC GGCCTCCTTA
4351 ACCCTCTCCT TCACCTACCA ACAATCCCGG AAGGACAACT CCAATTCCCT
4401 GCAGGTGAAA ACGTGCCACC TGGTCAGGTG AGTCTTTCCC CTGGGGCTCT
4451 AGCCCCTCCC CTTTCTCCCT TCTCTCTGGC TTCAGGCTGG CCTGGAGGAG
4501 GGGGCAGGGC GCTGTTTCTG GGAGTGGGTT TGAACCCTGG CTTGTCCGGG
4551 TGGGCAGTGC TGCCACAGGC TCACCCCTTC CTGGGTCTGG GCCTTAATTT
4601 TCTTTTCTGC GCAGTGCGGG TGGTTGTCTC AAGGGTCTAA TGTACACTTG
4651 GAGTGGCGAA GGAAAGAGCT GGAACCATAG TTTGAGGGTC TTTTTGCTTA
4701 GGTGACTATA ATCTCAAATA GCTCCTTGCA GCCTGCTGGG TGATGGTGGG
4751 GGAAGGGCTA TCTTGGGTGA CTCCCCGCTC CTCCAGGTAC TGGATCTCCG
4801 CCTTCCCAGC GGAGTTTGAC TTGAACCCGG AGTTGGCTGA GCAGATCAAG
4851 GAGCTGAAGG CTCTGCTAGA CCAAGAAGGG AACCGACGGC ACAGCAGCCT
4901 AATCGACATA GACAGCGTGT GCGTGGGGGG AGCACAGAGG GCTGGGGGGG
4951 CACTCAGTAT CCTATACCAT CTGTGCTTAA TAAATGTCTG TTGAACTGAA
5001 TGAGTGAGGG TCATGTTGCT CTCTCGCTTA AAAACCTTCC ATGGCTCCCT
5051 ATTGCCTTCA ACATGCCTCC TCTGGGCAGC TTGGCGTTCC TGCCTCATCT
5101 TCCACTGCCA CCACCCATCC CACACACCTC CTCCTGTAGC TGCGCTGGGT
5151 CGGCTCCCCG TCGGCTGAGC TCTCGAGTCC TTTCTCATCA TGGTGCTCTG
5201 CTCATATCAT CCCCCTTGCT GCCTCCTCCG TGTTACCAAG ACTCAGTTCA
5251 GGCATGAAGT CTCCGTGGGC TCTGAGGGTT CGGGGCTCTT CCGGGGTAGA
5301 ATTTGTCGTT CCCACCTCTG TTTTCCATGG CACTTTGTAC AGACTCCTGT
5351 ACAAAGACCT CTGTACATGT GTCACGCTGT TTTGTGATCA TGTGTTTCTG
5401 TGTCTGTCTC CCTCAGTAGA CTGTGAGCTC CTCGAGGGCA GGAACCGTGT
5451 CTTACTCATC TCTGTATTCC CAGCGCCTAG CACAGTGCCT GGCACAGAGT
5501 ACGTTGTTCA TAAATGTGTG TTGAGTGCAT GACGGGGTGG GGGGAGATGA
5551 GGAGGAGTTG CTGGGACTGG GAACATTCGT GCCTAGGACA GTGCCTCGCA
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FIGURE 3B

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5601 TTATGTAGGT TCTCAGTAAG CGTGAATGGT GTGTCTGTGT GAGTGGGGGG
5651 CCACGAGGCA TGCGCATGTC CAGCAAAGGG CTCACTACCC CTGCCCCCCC
5701 AGCCCTACCT ACAAGTGGAA GCGGCAGGTG ACTCAGCGGA ACCCTGTGGG
5751 ACAGAAAAAG CGCAAGATGT CCCTGTTGTT TGACCACCTG GAGCCCATGG
5801 AGCTGGCGGA GCATCTCACC TACTTGGAGT ATCGCTCCTT CTGCAAGATC
5851 CTGGTGCGGC CCGAGGGCTG GGGGGTCAGG GGTCCAATGT GGGCTGGAAG
5901 AGAGTTCTAG GAGGGGCAGG GTCCCTGGCG TAGGCTGGGT CACAGGGTGC
5951 ATCAGGGGTT TCAGTGTAAC CACTGAAGGT CAGCTGGAGG GTGAGGAGTG
6001 GCTATCAGTG AGGGGAGAGG CCGGCAAGGT GCTGAGGCCA CTCCTCATGC
6051 CCCCAGTTTC AGGACTATCA CAGTTTCGTG ACTCATGGCT GCACTGTGGA
6101 CAACCCCGTC CTGGAGCGGT TCATCTCCCT CTTCAACAGC GTCTCACAGT
6151 GGGTGCAGCT CATGATCCTC AGCAAACCCA CAGCCCCGCA GCGGGCCCTG
6201 GTCATCACAC ACTTTGTCCA CGTGGCGGAG GTGCCTGCCC CTCCCTCCCG
6251 GTGTCTCCCA ACCACCCCAC ATGCCAGTCA GGCCAACCCT TCCCTTCCCC
6301 TAACCCACTG CCTTCTCTCT AGATAAGCTG GGCCAAATTC TGGGCCCACT
6351 CAGTGACTCC CTGCCTCTCC GTCCCCATTT GCCTTCCAGA AGCTGCTACA
6401 GCTGCAGAAC TTCAACACGC TGATGGCAGT GGTCGGGGGC CTGAGCCACA
6451 GCTCCATCTC CCGCCTCAAG GAGACCCACA GCCACGTTAG CCCTGAGACC
6501 ATCAAGGTGC CTGGGACTGG GGAGGGGCCG GTGCTTCCCA GGTCTGTCTT
6551 CACTGGGTCC TCCCAGCAGC ACTGGGGGCT GGGCACAGCT GTCCTCATTT
6601 GATAGATATG GAAATGGAGG CTCAGAGGGG TTAAGTGCTT TTCTCAGTTT
6651 GCACAATGGC AACAGCAGAG TGGGGGCTCA CAGGTCGTCA GGGACCCCAA
6701 AGCTAGTACT TTTTTTTTTT TTTTAAGAC AGGGTCTCTC TCTCTGTTGT
6751 CCAGACTGGA GTTCAGTGGT GCAGTCACAA GCTCACTGCA GCCTTGAATT
6801 CCTGAGCTCA ATCGATCCTC CCACCTCAGC CTCCTGAGTA GCTGGGACTA
6851 CAGGTGTACG CCACCATGCC TAATTTTTGT ATTGTTATTA ATTTTTTTTT
6901 TTTTTTTTA GAGATGGGGT TTTGCCATGT TGCCCAGACT GGTCTTGAAC
6951 TCCTGGGCTC AAGTGATCCG CCTGCCTTGG CCTCCCAAAG TGCTGAGATT
7001 ATGGCTTGAG CCATTGTGCC TTGCCACTTG TAGTTTCTTC TTTTCTTTCT
7051 CCTTCATTTT TTATTATTTT TGAAGTATTT TGAAGTATTG AGTAACATAC
7101 ATATAGAAAA GTATATAAAA ACATATGAGA CTGGGCGTAG TAGCTCACAC
7151 CTGTAATCCC AGCACTTTGG GAGGCTGAGG TGGGCAGATC ACGTGACATC
7201 AGGAGTTTGA GACCAGCCTG GCCAACAAGG TGGAAACCCA TCTCTACTAA
7251 AATACAAAAA TTAGCCAGGC ATGGTGGCAC GCACCTGGAA TCCAAGCTAC
7301 TTGGGAGGCT GAGGCAGGAG GAGAATTACT TGAACTCAGG AGGCGGAGGT
7351 TGCAGTGAGC CAAGATTGTG CCACTTCACT CCAGCCTGGG CGACAGAGTG
7401 AGACTCCATC TAAAAAAAAA GAAAAGTATA TAAAAACATA TGAATAGTTT
7451 AAAGAAAAAT TGTAAAGAAA ACACTGTGTA ACTACTGCCC GGGTTGGGAA
7501 ATAGAACCTT GCCAGGCCCC CAAGCGCCCA GCACTTTAGA GCATAACTCC
7551 CTCCCCACGA CTTTTGCAAT GATGATCTTG CTTTTCTTTA TAGCTTCACC
7601 ATGTAGGTAT GCGGTCCAAA ACAATGTGGG GCTTTTTGTT GTCTGTTTTG
7651 AACTTTCTAT GAATGGAATG TTGTTTGTGT TATTTTATGT CTTGCTTTTT
7701 TCATTCCACA TGGTTCTGAG AGTCTTTTCA TTCTGTCATG TGGAGCAATT
7751 GTTTTTTCAT TTTCATTGCC ATATAATATT TTATTGTACG TCTACCCCAA
7801 TTCATTTATT TATTTATTTT TTTGAGATGG AGTCTGTCTC TGTCATCCAG
7851 GCTGGAGTGC GGTGGCGAGA TCTCATCACT GCAACTTCCG TCTCCTGGGT
7901 TTACGTGATT CTCGTGCCTC AGCCTCCTGA GTAGCTGGGA TTATGGGCTC
7951 GTACCACCAC GTCTGGCTAA TTTTTTGTAG AGACAGGCTT TCACCATGTT
8001 GCCGAGGCTG GTCTTGAACT CCTGAGCTCA GGCAATCCAC CCGCTTTAGC
8051 CTCCCAAAGT GCTGGGATTA CAGGTGTGAG CCACTGCCCC CAGCCTACCC
8101 CAATTTATGT ATTGATTCTA TTGTTGAATG TTGGGGTTTT TCCTTTTCTT
8151 TTCTTTCTTT CTTTTTCTTT CTTTTTTTCT TTTTTTTGGA GAGGGAGTCT
8201 TGCTCTGTCG CCAGGCTGGA GTGCAGTGAC GCTAATTTGG CTCACTGCAT
8251 CACTGCACCC TCTGCCTCCC GGGTTCAAGC GATTCTCCTG CCTCAGCCTC
8301 CTGAGTAGCT GGGACTACAG GCATGCACCA CCACACCCGG CTAATTTTTG
8351 TATTTTTTTA GTAGAGATGA GGTTTCCACC ATGTTGGCCA AGATGGTCTC
```

FIGURE 3C

```
 8401 CATCTCTTGA CCTCATGATC CATCTGCCAT GGCCTCCCAA AGTGCTGAGA
 8451 TTACAAGTGT GAGCCACCAC GCCCAGCTGG TTTTTCCAGT TTTTGCTGTT
 8501 TGGACGGGGT GGCTGAGTAT GTTCTTCCAG GTCATTGTCC TGTGCTGCCT
 8551 TGCCTCCCTG AGCCTCTGTT TCTCCTGTTA AATGTTGATG ATTCCCTGCA
 8601 TCCAGGCCTG GTTTAGAGGT GTGGTGCTTT TGGCAGTGAG TATTGCCTTG
 8651 AATTCATGGC AATGAATTCA ATCCCCAGGG GCTGAGAGAG CCAGTCGTGG
 8701 GGGACAGTAA GGGAGGTTTT TACTCTTTCA CCTGTCCCTG ACCCTGACTC
 8751 CTCCTCACCC CCTCCTACAT TTCCAGGGCT GAGGTAGGGA GGATAGTTGT
 8801 GGGGGTATGA CTCCTCTGTC CTTTGTCCCC AGCTCTGGGA GGGTCTCACG
 8851 GAACTAGTGA CGGCGACAGG CAACTATGGC AACTACCGGC GTCGGCTGGC
 8901 AGCCTGTGTG GGCTTCCGCT TCCCGATCCT GGGTGTGCAC CTCAAGGACC
 8951 TGGTGGCCCT GCAGCTGGCA CTGCCTGACT GGCTGGACCC AGCCCGGACC
 9001 CGGCTCAACG GGGCCAAGAT GAAGCAGCTC TTTAGCATCC TGGAGGAGCT
 9051 GGCCATGGTG ACCAGCCTGC GGCCACCAGT ACAGGCCAAC CCCGACCTGC
 9101 TGAGCCTGCT CACGGTGAGG AGCAGGGGGC AGGGAGGTGG GGAGCTGGGC
 9151 ACCAGGGGTT GACAGTTTCC CCAGGTCCTG GCTGTGGGCG TGGCCTGGGG
 9201 CTCTGGGTTC TGGCCAAGAA ACTGAGATCT AGCGTGGGCT CTGGGGTTTG
 9251 GAGTGGATGC TGAGAAGGGG TCCAGGCTCT GGTTGGGGCT GTGGACTGAG
 9301 GTCTGATCTC CAGGCTGGTA TGTGGACTGT GGGCAGTTTG AACTGGGCCT
 9351 GGGTCCCGGG TTGAGTTCTG GCAATGGGCT GTGTTCTAGG CTGGGCCAA
 9401 GCTCTGCATT CTGTGGGCAG GGGTGGTTTC TAAGCATGGC CCTGGGCTCG
 9451 GAGTGAAGTT CTGGGCTTGG CTTTACACTT GGTCTTGGGG TCTAGGGTGG
 9501 GAGTTGGGTT CTGGTTTAGA TCCAGACAAG GTTCTAGACA TTGGGCTGGG
 9551 GCTTAAGTGT TAAGGTTTGG AGTGGATTCT TAGCTGCTTC TGGGCTCTGG
 9601 AGGGGATCAG GGTTGAAATC AGAGCTTCTG GCTGGGTTCC GACCTGGCTT
 9651 CTTCCCTGAC ATCTTGGCAA TATGTTGTGT TCAAGGTTTG GGGCCATGCT
 9701 GTGGTTTGAT CTGTGCGCTG GGATGACATG GGGGTTGCTG TGCTGTGTTC
 9751 TAAGCCAGGC TTTGTCCTGA GTCTAGCTTC TGACCCGAGC TCTGGCTGAG
 9801 CTGTGGCCTC TAGGTCGACC TTTGGCCCTG GGCTCTGTGG CCGTGGGCAG
 9851 GGGCCAGTGG GGGTGATCAG ATCTGTGTGT CCCAGGTGTC TCTGGATCAG
 9901 TATCAGACGG AGGATGAGCT GTACCAGCTG TCCCTGCAGC GGGAGCCGCG
 9951 CTCCAAGTCC TCGGTGAGGG GGTACTCCCT CCTCTCCACT CTGCCCTTCC
10001 CTCCTGAGAA TCCCAGGATG TGAGGATGGG AAGAGCTCTT AGCAGCCACC
10051 TCACCCATCC ATCTTGTAGG ACAGAGGCAT CCTGGGGGTA GGGCAGTAGT
10101 GTTGGGCAGA CTTCCCTCTC CCAGGGATTC CCCTCTCTGT TCCCCGGGGC
10151 TCTGGGCTCC CCCTGCCTCT GGCCCTAGCT CAGGCCCGAC CATTTCCATA
10201 GCCAACCAGC CCCACGAGTT GCACCCCACC ACCCCGGCCC CCGGTACTGG
10251 AGGAGTGGAC CTCGGCTGCC AAACCCAAGC TGGATCAGGC CCTCGTGGTG
10301 GAGCACATCG AGAAGATGGT GGAGGTGAGC TCCTGCGGAG CCTGAGCAGT
10351 GTGTGGGGAG AGGCCAGTTT GCCGGAGCAC TGCCCTGGAA GCCAGCACGA
10401 GTGTCCTGTT CAAGACCCAG CACTCAGCCC CTAGGAGTCA CAGGGCCTGG
10451 CAGGCCAGCT GCACGGGGCT GAAGTGCCCC TGGGTAGGGT GGGGGTGGAG
10501 GTATGGAACG GGGGTGGTGT CAGAGACCTC TCTGAGACAC ACCTCATCAA
10551 ATGGACTGGG AACGTGGGAA GGGACAGGAC CTGATGTCCC CTTTACTCTC
10601 CCCTCTTCTG GCTCTGCGTG TCCCTCTGCG TGCCCCAGTC TGTGTTCCGG
10651 AACTTTGACG TCGATGGGGA TGGCCACATC TCACAGGAAG AATTCCAGAT
10701 CATCCGTGGG AACTTCCCTT ACCTCAGCGC CTTTGGGGAC CTCGACCAGA
10751 ACCAGTGAGG AGGGCTGGGG ACCTGGGGGA GAGGGAAGGC AACTCAGCCC
10801 ACTTCTGCCT GGGCTTCAGT TTCTTGTGTG CAAGATGAGG TCACTGAGCC
10851 AGATGATCTT GGCCTGGGAA GCTGCCAGTG TGGGAAAGGG CACTTGCTTT
10901 TGTGGGGAGG AGAGGCTGCC AGCTGTGGAG GCGCAGTGGT ATCTCACAAA
10951 TTCAGACAGA TGGGGGGCTC CACCTGAGTC TTGCAAAGAC TGTGACCTGG
11001 GGACTGTGGC TACAAAAGTG CTGTTTTATT TGTGGAGCTC ACAGCTGTCA
11051 AGAAGTGTGG GCAACTTGAG CTCCTGGATA GTCTGTTCTA ATGAATAGAT
11101 AAGAAAGGTT TGTAATTAGC AGTACCCAGT TGTTTATCAA CAGTTCATAT
11151 GCTGACAATT TGGAAAAACA GCTGGTTCTC TGAAGTAGGT TAAACATGCC
```

FIGURE 3D

```
11201 CCCTGAAGCC AGATTCATGC CCTATTTTTG CTGAGCAGAA AAAACTCCAT
11251 TCAAAATTTA AAGTCCATCT CAGGTCGATT TATTTTTTAA TGTTACCTGT
11301 ATTTCAAAAA TCTGTTGTTT TTTATTTCCA CATTACAAAA ATCCACGGTA
11351 AAATAAAATC TAGGTGGTAA AATAAATTTA TAGTGAACAA AATGTTTAAA
11401 GTAAGAAGTG AGAGGCCAGG TGCGGTGCCT CACGCCTGTA ATCCTAGCAC
11451 TTTGGGAGAC TGAGTTGGCA GGATCAATTC AGGCCAGGAG TTTGAGCCCA
11501 GCCTGGGCAA CAGAGTAAGA CCCTGTCTCT ACAAAAATTA TTATTATTAT
11551 TTTTGAGACA GAGTCTCACT CTGTTGCCCA GGCTGGAGTG CAGTGGTACA
11601 ATCTCGGCTC GCTGCAACCT CCACTTCCTG GGTTCAAGTG ATTCTCCTGC
11651 TTCAGCTTCC TGAGTAGCTG GGATTACAGG CATGCATCAC CGTGCCTGGC
11701 TAATTTTTGT ATTTTTAGCA GAGATGGGGT TTTACCATGT TGGCCAGGCT
11751 GGTCTCAAAC TCTTGACCTC AAGTGATCTA CCTGCCTTGG CCCCCCAAAG
11801 TGCTAGGATT ACAGGCATGA GCTACTGCTC CTAGCCTAAA AAAATTTTTT
11851 TTGGGCATGG GTGGCACGTG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG
11901 GCAGGAGGAA CCCTTGAGCC CAGGAGGTTG AGACTGCAGT GAGCTGTCAT
11951 CACACCACTG CACTTCAGCC TGGGTGACTG CGCGAGATCA CCCCCATCAA
12001 AAAAAAAAAA AAAGAAAAA AAAAGGAAGA AATGAAAGTC CCCTCTTTCC
12051 TTTTCCACTG GTAGAAGTTG CCATGATTAA GCACTGTTAA CAATATTAAG
12101 CTTGGCAGTA TGTGGATTCT TCCAGTCTTC TTTTCCCAGG CAGGTGCACA
12151 TTGATAGAGA TTTTGTTTGT TTGGTGTCTG TTTCATGGAC AAACAGGATT
12201 AGAGCATAAA TCTAGTTCTG CTTGTGGCTT TTATCATAGC TGCTTTATTT
12251 CTTCTCCCAG ATTTTAGGCA GAGGTAGTTG AGTTCCATGT TTTCTCCCTG
12301 GGTTGGTGGG TGGATTTTTA TCTAGACCAC CTTTTCAGTG AGAATGACCC
12351 TTTGAGACGA TGGAGGCCTC AGCTTCATGC AGCGGGCTCA GCCTTAACCC
12401 TCCACCTCCT GCAGGCCCCA AGCTGTGTGT GTGTGTGTGT GTGTGTGTGT
12451 GTGTGTGTGT GTGTGTGTGT GTTGGTAAGG GGAAAGCCCC TGGTTGGGTA
12501 TCAAAAACCT AGCACCTGGT TCGGCAGGAG GGAGACCAGC ACCGGCTCCC
12551 CAGGACCAGG CCCAGCTCAC CACTTCATTG TAAAGCTCCC TCTTTGTTTC
12601 TGGAACTTGG GTGTTTCCAT TTCTTTCTTA CAAAATTATC TATGCATTTA
12651 CAGCAATTGT TGATATATCT TTAGGCAGCA TCTAGGTACT TGTAGTGGGT
12701 TCTCTTTTTT CTTTTTTCTT TTTTTAATC ACCCTCTCTT TTTTTTGAGA
12751 CAGAGTCTCA CTCTGTCGCT CAGGCTGGAG TGCAATAGCG CGATCTTGGC
12801 TCACTGCAAC CTCTGCCTCC CAGGTTCAAG TAATTCTCAT GCCTCAGCCT
12851 CCCAAGTAGC TGAGATTACA GGCACTGGCC ACCAGACCCG GCTAATTTTT
12901 TTTTCTTTTT CTTTTTTTTG AGACGGAGTT TCGCTCTTTG TTGCCCAGGC
12951 TGGAGTACAG TGGTGTGATC TCGGCTCACT GCAACCTCCG CCTCCCGGGT
13001 TCAAGTGATT CTCCTGTCTC AGCCTCCCGA GTAGCTGGGA TTACAGGCGC
13051 GCGCCACCAT GCCTGGCTAA TTTTGTATTT TTTTTTTTT GAGACAGAGT
13101 CTCACTCTGT CACCCAGACT GGAGTGCGGT GGCGCGATCT CGGCTCACTG
13151 CAAGCTCTGC TTCCCGGGTT CATGCCATTC TCCTGCCTCA GCCTCCGGAG
13201 TAGCTGGGAC TACAAGCACC CACCACCGTG CCCGGCTAAT TTTTTGTATT
13251 TTTAGTAGAG ACGGGGTTTC ACCGTGGTCT CGACCTCCAG ACCTCGTGAT
13301 CCACTAGCCT CAGCCTCCCA AAGTGCTGGG ATTACAGGCG TGAGCCACCT
13351 CACCCAGCCT AATTTTGTAT TTTTAGTAGA GATGGGGTTT CACCATGTTG
13401 CGCAGGCTGG TATTGAACTT CTGACCTCAG GTGATCCGCC CGCCTCGGCC
13451 TCCCGAAGTT CTGGGATTAT AGGCGTGAGC CACCGCACCT GGCCTAATTT
13501 TTGTATTTTT AGTAGAGATG GAGTTTTACC TTGTTGGCCA GGCTGGTCTT
13551 GAACTCCTGA CCTCACCTCA GGTGATCTGC CCACCTCGGC CTCCCAAAGT
13601 GCTGGGATTA CAGGCATGAG CCACTGTGCA CCCGGCCTAA AAATCACCAT
13651 CTTGACAGAA CTTCACGCCT TGCTTTTTGT TTTTTTTCAT CTTTGTGCTT
13701 GTTTTCCACT TAACCCTTGA TCACAGACAT CTTTCCATGT GGATTCATGT
13751 AGAACTACCT CATTCGTTAG AACAGCTGCA GAGTATTCCA CTGTGCGGTT
13801 AGTCCATCAT TTCCCTAACC ATCCTCCTGC TGATGGACAG TTAGACTGTT
13851 CCAGTTTTTC AGTATGATTC TATGCCAGGC TGCCATGAAC GTCCTTTTAC
13901 TGATCCACTC AGGCCAGTAT TTCTGTAGGA GAAATTCCTA GAAGTGGGAT
13951 AATTGGATCA AAAGATATGC ACATTCTAAA TTAGGAGAGA GACTGCCAAA
```

FIGURE 3E

```
14001 CTGACCTCAG ACAAGGTTGT ACCAGTTTGC ACCCCCATCA GCAGCGTACA
14051 AGTGCCTGCT TCCCAACTTC CTCGCCAACA GGGATGCTAT AAAAAGCTTC
14101 ACAATTTTGC CAGTCTCATT GGCAAATGGT ATCTTGGTTA AATTTGCATT
14151 TCTTTAATAC TAAGTGGGGG TAGGGTATCT TTTCATATGT TTATTGGCCA
14201 TTTATTTCTT CTGTCAATTG CCTGTTCTGA TTCCTTGTCC ATTATTCTAC
14251 TGGGTTGTT GGTCTTTTTC TCATTGATTT TTAGAATCTC TGTTAATGGA
14301 TATTAACCCT TTGCTGTTGA ATGTGTTTGC AAATATTTTC TCCCTGTCTG
14351 TCATTTATGT GTCTTTTTCC ATATAAATTT AAAAAATTTT GGTGGGCTCA
14401 ATAGGTCAGT CTTTCCCTTC CGGGCTTCTG GGATTTGTGT TCGGGGTAGA
14451 AAGGCCCTCA GCCCCTCAAG ATTATAAAAT TATAAAACCT TTTCTTTTTT
14501 TTTTTTTTTT CTGAGACAGG GTGTCTTGCC ATGTCACCCA GGCTGGAGTG
14551 CAGTGGCATG ATCTTGGCTC GCTGCAACCT CCACCTCCCA GGTTCAAGTG
14601 ATTCTCGTGC CTTAGCCTCC CGAGTAGCTG GGATTATAGG TGCCTGCCAC
14651 TATGCCTGGC TAATTTTTTG TATTTTTAGT AGAGACGGGG CTTTGCCATG
14701 TTGGCCAGGC TGGTCTTGAA CTCCTGACCT CGTGATCCAC CCGCCTTGGC
14751 CTCCCAAAGT GCTGGGACTA CAGGCGTAAG CCACTGTGCT CGGCCCTATA
14801 TTTTTTTCAG ATAGCCAGTT ATCCTAATGC TCCCTTGATT TGATGGACCA
14851 CCTGGATCAC ACATTATGAG CCCCCTCATA AGCAGGTGGG AGTCTCAAGC
14901 GAGGGCCAGT CCCGATGGGA ATAGCACTTG GTGGCTGAGG ACCCTCCTAT
14951 CTGTGCAGAC ACTGTTGTAA AACTTCACAT GCATCATCTA ATTTAGTCCT
15001 CACCAAAATC CTATGAAATG TAGGAATGAT CATTACACCC ATTTATAGAT
15051 AAGGAAACGG AGGGACAGGG AGATTACTCC GCTACAGGTC AAGAGGCAGG
15101 GAAGTAGAGC TGCGATTTGA ACTGAGGTCT GTGTCTAGAA CACGTGCTCA
15151 TTCTTTCCCT AAAATGTATT CATAGGTGAA AAAGGGCTTC TGCGGAAAGC
15201 CCTGGGTTAT GTGGGAAACC CTGGATTTAC AGCTGTCTTT CCAGCAGGAT
15251 GATGCAGGAG AGAGAGGGAT GCGATTTCTC CCAATCTCTC CTGGTCCCAG
15301 AACTCATTAG AGAGTTCTCC CTGCTGAGGG CTCCCGACTG GTGTTGCACA
15351 CAGTACACTT CGGGAGCCCG AGGCTGATGG TTCCATGGAA AGTACACAGT
15401 CATTTTAGTT TGCACACCAA GTGTGAAGTG GGCAGGACAG GCCACTGTTC
15451 TGAGAAGGAA CCCAGGGAAA GGGACTGGCC CAAGACCACA CACTGGTTAG
15501 CGGCACTTCC CACATCTGCC TGACCCCTAG TCCAGTGCCG CCTTTTCTTT
15551 ACTCTGCAAC AGGAGTCCAA AATCAGGAGT TCCATGAGGA CACTGGGAAC
15601 AGTGGGATGG GTTAGGCCAG CGGTGGATGG TTCTGGGGAG GGCCCGAGCT
15651 GAAGCGCCCC CGCAACTCCC CACAGGGATG GCTGCATCAG CAGGGAGGAG
15701 ATGGTTTCCT ATTTCCTGCG CTCCAGCTCT GTGTTGGGGG GGCGCATGGG
15751 CTTCGTACAC AACTTCCAGG AGAGCAACTC CTTGCGCCCC GTCGCCTGCC
15801 GCCACTGCAA AGCCCTGGTG AGAGTCCCTT TCCCGGCTCA CGGCCCAAGC
15851 CACGCCCCTC CAGCCCCGGC CCCGCCCTCC CTTCTGGCCC CGCCTCTGCC
15901 AGAGCCCTTC TCAAGCCAGG AAAACCTGGT AATTCTATTT GCCTCTCCTC
15951 CTGTGGTTCT GCCCGGGGCC CTGAGGCGGG CTCTAAAGCC CTAGTCTCAC
16001 CCTCAAGAAG GAAGAAGTAG AGTCATCACC TCTAAATCCC TCCTCCCACC
16051 ACGGCCCCTC CTCTATTGCA GATCCTGGGC ATCTACAAGC AGGGCCTCAA
16101 ATGCCGAGGT GAGATGGAAT GACTGGAAGG GCTGCTGGGC AGTGTTTTTT
16151 TTGTTTGTTT GTTTGTTTGG GAGAGTTACT ATTTTGGTGG GGCAATTGCC
16201 AAGGAGTGAA GTACCTTAAA ATCAGAGGCG CATGGCCGGG CATGGTGGCT
16251 CAAGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGCGCGC AGATCACCTG
16301 AGGTCAGGAG TTCAAGACCA GCCTGACCAA CATAGCGCAA CCCCGCCTCT
16351 ACTAAAAATA CAAAAAGTAG CTGGGCGTGG TGGCACCCAC CTGTAATCCC
16401 AGCTACTTGG GAGGCTGAGG CATGAGAATC GCTTGAACCT GGGAGGCGGG
16451 GTTTGCAGTG AGCCGAGATC ACGCCACTGC ACTCCAGCCT GGGCAACAGA
16501 GAGGGCTCTG TCTCAAAAAA AAAAAACAAC AAAAAAACCC CCAAAACCAA
16551 AACCCCACAA AATCAGAGGC TCAAGATGAC TGATGTGAAG GGAGTGGCGT
16601 TTAAGAGGCC ATTTATTTTG ATGACGCAGC TGCCCAGGAA CAGAGAACAT
16651 GGGAGAAGGC ATAGACTGAC AATTAGGAGG AGGAGAACAC TTTGGAAGGA
16701 GACTCTTATT TTGGTGGGGC AGCTGCTCAG GAACAAAGGT TCCTGGTAGG
16751 GGGGCGCAAG CCTGCGGGAT GGGATGGAGG GTATTCTGAC CAATGTCCCT
```

FIGURE 3F

```
16801 GGCTGGCTCT CCATTTGCTC TCCCCCAGCC TGTGGAGTGA ACTGCCACAA
16851 GCAGTGCAAG GATCGCCTGT CAGTTGAGTG TCGGCGCAGG GCCCAGAGTG
16901 TGAGCCTGGA GGGGTCTGCA CCCTCACCCT CACCCATGCA CAGCCACCAT
16951 CACCGCGCCT TCAGCTTCTC TCTGCCCCGC CCTGGCAGGC GAGGCTCCAG
17001 GCCTCCAGGT AAGAGGGAGT CATTCTGTAC TGGCCTGTGG AGGGAAGGAT
17051 GCAGGGCTAC TGGGGCAAAG AACGCAGGAT GGAAGCCATT CCAAAGTGCA
17101 TAATTCTCTT TTTGTGGTGG GATAATAAAG AAGGGACAGG CCGGGCGCGG
17151 TGGCTCACGC CTGTAATCCC AGCACTTTGG GAGGCCGAGG CGGGCGGATC
17201 ACGAGGTCAG GAGATCGAGA CCATCCTGGC TAACACGGTG AAACCCCATC
17251 TTTACTAAAA ATACAAAAAA AAAAAATTAG CCAGGCGTGG TGGCGGACGC
17301 CTGTAGTCCC AGCTACTTGG GAGGCTGAGG CAGGAGAATG GCATGAACCC
17351 GGGAGGCGGG GCTTGCAGTG AGCCGAGATC GCGCCACTGC ACTCCAGCCT
17401 GGGCGATAGA GCAAGACTCC GTCTCAGAAA AAAAAAAAAT AAAAAATAAA
17451 GAAGGGACAG GTAAGGGTGC CAGAAAGTGG CCAGGAAGCC CTGGACCTTC
17501 TGAGGCTGAG GAGAGAGACC CTAATTTATA AAGAGGTATA AAAGTGAAAG
17551 AGGCTTCAAG ATTCCAGTTA CAGTCTTATT TTGTTGGAGG GGTTAACAAA
17601 GGATTGGAGA AGGTGTTATA TGAGCCATTG GCTTGCCTTT CCCTTTCTGG
17651 CTGCTCTGGA GGCTCTTCTG GGGAAAGTCC CTTGCCCTGA TAATGTCCTG
17701 GCAGCTCTCT TGGGGTATTT GATGGTTTTA GGTCAGTTTG CTGAATGACA
17751 ACTGGCCAAA TGATTATTTT GCTGAGAACA GTCCGAACAA CTATGTTAAA
17801 CTGGGGTCTA AGGTAGTTGA TCACAACTGT TTGGGTTGGC ATAAGTCCTC
17851 AAAAAACAGA GGCAGGCACA GGGCATACAT CCTCAAAAAT AGAAAGATA
17901 AATCCATTTG CATTGAGCCT TCCAGAAGTG CTGGGGTCTA AAATGTGAAA
17951 TACACACAAA ATTGACATTT AAGCAAACTG CGCTGACAAA TCTGTGGCTG
18001 AAAAAGCTGT GGCAAAACAA AAACATAGAA AAAGAGCCTC AAAAATTGGG
18051 CTGAGGCCAG GCATGGTGGC TCACGCCTGT AATCCTAGCA CTTTGGGAAG
18101 CCAAGGTGGG TGGATCACCC GAGGTCAGGA GTTGGAGACC AGACTGGCCA
18151 ACGTGGCAAA ACATCATCTC TACAATACAA AAATACAAAA ATTAGCTGGG
18201 CGTGGTGGCA GGCGCCTGTA ATCCCAGCTA CTTGGGAGGC TGAGGCACGA
18251 GAATCGCTTG AACCTGGGAG GTGGAGGTTG CAGAGAGCCG AGATTGCGCC
18301 ATTGCACTCC AGCCTGGGCG ACAGAGAGAG ACTCTGTCTC AAAAAAAAAA
18351 AAAAAAAAAA AAATTGGGCT GTGAGGTCAT GCAGGGAATT GATTTTTGGT
18401 GGGTGGGTCT GCTTCTGGGA TGATGTGGAT GCCTCCGTG GAGAGGGGAA
18451 GGGTTGATGA AGTCCCAGGG ACCTGGAAGT GTGTTCTGCA GCAATCCCCC
18501 TCCCAGCAGA GATCCGTGAG GAGGAGGTAC AGACGGTGGA GGATGGGGTG
18551 TTTGACATCC ACTTGTAATA GATGGTGAGT CCTCCCACAG CTGGCACCAG
18601 AGCTCCCCAC TGAGGGCTGG GGGGGAGCTG GGGAGTATCA GGGAAATGGG
18651 TGCTTTATCC AAATGGCTCC AAGCCAGGTG GGCTACTACC TTGTTGTTAG
18701 GGGGGTGTCT TCCTCACAAC CTGTTTTTCT CTTCCCAGCT GTGGTTGGAT
18751 CAAGGACTCA TTCCTGCCTT GGAGAAAATA CTTCAACCAG AGCAGGGAGC
18801 CTGGGGGTGT CGGGGCAGGA GGCTGGGGAT GGGGGTGGGA TATGAGGGTG
18851 GCATGCAGCT GAGGGCAGGG CCAGGGCTGG TGTCCCTAAG GTTGTACAGA
18901 CTCTTGTGAA TATTTGTATT TTCCAGATGG AATAAAAAGG CCCGTGTAAT
18951 TAACCTTCAC CATCAGCGCC TAGAATCCCG GGGGGTAGGG GGATGGTATA
19001 CTTTACAGGA TGACAATCTT GGGAGCTAGA ACTTTGTAGC CAGAGAAACT
19051 TGGGAGGTCT GGAATCTCAT GTGTCTGGAG TCTTGGGGAA GAGAATCTTA
19101 GAAGCAGAAA ACCTTGGAAC ATAAGAATCT TGGGGAGGGT CTAGGATCTT
19151 GAGGAGACCA GATCCTTGGA CATCTAAAAC TTGAAACTAG TAGGTCTGCA
19201 CCCGAGAATT GCAGGGCCAG TCATGCATAC CCAAAGCCTT CAGCCCATGG
19251 CCGAAATTCC CTTGCTGGAC AGGGGGCCTT TCAGCCCCTG CTTGGACGCT
19301 TCCAGTAACA GGGCCCTCAC TGCAGGAATC GTGGGAGGGA GAGGGGCAGC
19351 ACAGAGTTGC TGGCTGTCGG GGAAGGGAGG GAGGGCCCTG GGCAGTCCGA
19401 GGGCCCTGCT GGGCTTGTGC CTCAGGGTGG GGGCTGCACT CCTCCGCCTT
19451 GCAGCCTCCT GGCCTGGTGC TGCTGCCAGC CGGAAGGACA GTGACTTCCA
19501 GAGGAAATGC ATATTGATCC TGCTTTCAGC CTCCGGTGGT GGCTTCTCCC
19551 AACCCAGCTC TTCCCTCCTG AGCCTGCAGC ACGGAGGTTT TGGGGGTCAC
```

FIGURE 3G

```
19601 TGCTACCTAA AGAAGGCTAA GGCCACTTCT GAGGCTGGTC TGGGAGTTTA
19651 CTAAAGGTTC TGAAGCTGGG CCGGGCTGCC CCTGGGATCA GGAGACTCCA
19701 GACAGCAGTC CTGACAATGG GAACTACCTC CTCAGTCCCC CAAACTGGGA
19751 GGTGTCCCAC AGCAGCTGTA GGATTGTCCT AGGGGTGGAG ACCTGAGCAC
19801 CTTCCACTCC AAAGCACAGT ATCTGTGGGC CTGGCAGTGG CCTCAGTTCC
19851 CCCATGAGTG CCCCGGTCCC CCACCCCAGG GTTTCCCCAC ATCACATCCA
19901 TCCCTGCTTT GAGACCCCAC TCCCCCTGGC CTGTTCTTTA TTTTGGGTCA
19951 CTCCCTTCTC TTTCCTGGTC ATATCTCTCC TGCAGGCCTA CCCTGTGTTG
20001 GGCCCCCCAG CCCTGTCTCT GCATCGGGTG CCCCCCTGCC CCTCCTTCTG
20051 TCCTCAGCCC CCTCCGCCCT TCCCCCTCTT GAGGCTGTAA TATCCGTTTC
20101 ACGATTTGGG GGCTGAGTTG CTATAACAAC AGACGGCGAT TGTGTTGTGA
20151 AGAGCAGCTC GCTCCTGTGC CGCCTGCCTC CTGTGCTGCC TCCATCCCTG
20201 CAGCCCAGTC GGTTCCTCTT GGCTCCTCTC GTCACTACCC TCCAGTTCCA
20251 GTCTGGCCTC TTCCTGGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTAT
20301 GCATGCATGC ATATGTGTGT CCAGGTCTGC CTGCCCGGGA TGTGACAAGT
20351 AGCGGTCTTC ATGGTTGCAT GTGTCTGAAT TTGGTGTCTG AGCTTCACAT
20401 TGTATGCGCC TGTGTGCATG TGTGTGCATG GACATGCATG CTGTATCTGC
20451 TGTGTTTCCC CTCCCCCATG TGTCCCCACT GGCCTTTGCA CATGGGAGAA
20501 GGGCATGTGC TCAGCATATC ACTCAACTGT CCACATTGGG TGGGTACCTG
20551 TGTGTGGTGT GTGTGTGTGG GGGGTGTGTC TTGAAGTGGC AGGTCCCAAA
20601 TGCTTAGGCA ATCTGAACCT TGGACCTTGC AGAGAGGAGA GATGTCCCTG
20651 TAGGTGGGAG GGACAGGGAG ATGCAGCAGC TGCCCGGTGA CCTTTTCTGC
20701 CCTTGATGGG CAAAGCTGGG GGTAGGGAAA GGAGACAAGT GCTCATACTT
20751 ACCTCCCTCC CTGCCCAGGC TCCTCTGTAA GGGTCTGAGT CTGTCTCTGT
20801 GAGCCATTGC ATCTGTCTGT CTATGCCCTG ATGCCTGGAT GGACAAGGGG
20851 TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG AGTGTGAGGC TGCAGGAAGA
20901 GGAACAGTGG GGGATGGGCA GGAAAGTGGG CTGTGGGGTC AGGGAGGCGA
20951 T   (SEQ ID NO:3)
```

FEATURES:
```
Start:    3000
Exon:     3000-3072
Intron:   3073-3753
Exon:     3754-3855
Intron:   3856-4363
Exon:     4364-4427
Intron:   4428-4786
Exon:     4787-4918
Intron:   4919-5702
Exon:     5703-5853
Intron:   5854-6056
Exon:     6057-6230
Intron:   6231-6389
Exon:     6390-6506
Intron:   6507-8832
Exon:     8833-9114
Intron:   9115-9885
Exon:     9886-9963
Intron:   9964-10201
Exon:     10202-10324
Intron:   10325-10638
Exon:     10639-10754
Intron:   10755-15675
Exon:     15676-15817
Intron:   15818-16071
```

FIGURE 3H

```
Exon:    16072-16108
Intron:  16109-16828
Exon:    16829-17008
Intron:  17009-18491
Exon:    18492-18565
Stop:    18566
```

CHROMOSOME MAP POSITION:
Chromosome 11

ALLELIC VARIANTS (SNPs):
DNA

Position	Major	Minor	Domain
5539	C	G	Intron
5658	T	G	Intron
5861	C	T	Intron
6023	A	G	Intron
6799	C	T	Intron
9579	C	A	Intron
9842	T	C	Intron
10159	T	C	Intron
12025	A	- G	Intron
14723	T	C	Intron
14996	G	A	Intron
16153	T	G	Intron
16181	G	A	Intron
16756	A	G	Intron
18059	A	G	Intron
18364	A	- T	Intron
18861	G	A	Beyond ORF(3')
20443	G	A	Beyond ORF(3')
20881	A	T	Beyond ORF(3')

Context:

DNA
Position

5539
AGACTCAGTTCAGGCATGAAGTCTCCGTGGGCTCTGAGGGTTCGGGGCTCTTCCGGGGTA
GAATTTGTCGTTCCCACCTCTGTTTTCCATGGCACTTTGTACAGACTCCTGTACAAAGAC
CTCTGTACATGTGTCACGCTGTTTTGTGATCATGTGTTTCTGTGTCTGTCTCCCTCAGTA
GACTGTGAGCTCCTCGAGGGCAGGAACCGTGTCTTACTCATCTCTGTATTCCCAGCGCCT
AGCACAGTGCCTGGCACAGAGTACGTTGTTCATAAATGTGTGTTGAGTGCATGACGGGGT
[C,G]
GGGGGAGATGAGGAGGAGTTGCTGGGACTGGGAACATTCGTGCCTAGGACAGTGCCTCGC
ATTATGTAGGTTCTCAGTAAGCGTGAATGGTGTGTCTGTGTGAGTGGGGGGCCACGAGGC
ATGCGCATGTCCAGCAAAGGGCTCACTACCCCTGCCCCCCCAGCCCTACCTACAAGTGGA
AGCGGCAGGTGACTCAGCGGAACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTGT
TTGACCACCTGGAGCCCATGGAGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCCT

5658
CCTCTGTACATGTGTCACGCTGTTTTGTGATCATGTGTTTCTGTGTCTGTCTCCCTCAGT
AGACTGTGAGCTCCTCGAGGGCAGGAACCGTGTCTTACTCATCTCTGTATTCCCAGCGCC
TAGCACAGTGCCTGGCACAGAGTACGTTGTTCATAAATGTGTGTTGAGTGCATGACGGGG
TGGGGGGAGATGAGGAGGAGTTGCTGGGACTGGGAACATTCGTGCCTAGGACAGTGCCTC
GCATTATGTAGGTTCTCAGTAAGCGTGAATGGTGTGTCTGTGTGAGTGGGGGGCCACGAG

FIGURE 3I

```
       [T,G]
       CATGCGCATGTCCAGCAAAGGGCTCACTACCCCTGCCCCCCCAGCCCTACCTACAAGTGG
       AAGCGGCAGGTGACTCAGCGGAACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTG
       TTTGACCACCTGGAGCCCATGGAGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCC
       TTCTGCAAGATCCTGGTGCGGCCCGAGGGCTGGGGGGTCAGGGGTCCAATGTGGGCTGGA
       AGAGAGTTCTAGGAGGGGCAGGGTCCCTGGCGTAGGCTGGGTCACAGGGTGCATCAGGGG

5861   CTGGGACTGGGAACATTCGTGCCTAGGACAGTGCCTCGCATTATGTAGGTTCTCAGTAAG
       CGTGAATGGTGTGTCTGTGTGAGTGGGGGGCCACGAGGCATGCGCATGTCCAGCAAAGGG
       CTCACTACCCCTGCCCCCCCAGCCCTACCTACAAGTGGAAGCGGCAGGTGACTCAGCGGA
       ACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTGTTTGACCACCTGGAGCCCATGG
       AGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCCTTCTGCAAGATCCTGGTGCGGC
       [C,T]
       CGAGGGCTGGGGGGTCAGGGGTCCAATGTGGGCTGGAAGAGAGTTCTAGGAGGGGCAGGG
       TCCCTGGCGTAGGCTGGGTCACAGGGTGCATCAGGGGTTTCAGTGTAACCACTGAAGGTC
       AGCTGGAGGGTGAGGAGTGGCTATCAGTGAGGGGAGAGGCCGGCAAGGTGCTGAGGCCAC
       TCCTCATGCCCCCAGTTTCAGGACTATCACAGTTTCGTGACTCATGGCTGCACTGTGGAC
       AACCCCGTCCTGGAGCGGTTCATCTCCCTCTTCAACAGCGTCTCACAGTGGGTGCAGCTC

6023   GGCAGGTGACTCAGCGGAACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTGTTTG
       ACCACCTGGAGCCCATGGAGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCCTTCT
       GCAAGATCCTGGTGCGGCCCGAGGGCTGGGGGGTCAGGGGTCCAATGTGGGCTGGAAGAG
       AGTTCTAGGAGGGGCAGGGTCCCTGGCGTAGGCTGGGTCACAGGGTGCATCAGGGGTTTC
       AGTGTAACCACTGAAGGTCAGCTGGAGGGTGAGGAGTGGCTATCAGTGAGGGGAGAGGCC
       [A,G]
       GCAAGGTGCTGAGGCCACTCCTCATGCCCCCAGTTTCAGGACTATCACAGTTTCGTGACT
       CATGGCTGCACTGTGGACAACCCCGTCCTGGAGCGGTTCATCTCCCTCTTCAACAGCGTC
       TCACAGTGGGTGCAGCTCATGATCCTCAGCAAACCCACAGCCCCGCAGCGGGCCCTGGTC
       ATCACACACTTTGTCCACGTGGCGGAGGTGCCTGCCCCTCCCTCCCGGTGTCTCCCAACC
       ACCCCACATGCCAGTCAGGCCAACCCTTCCCTTCCCCTAACCCACTGCCTTCTCTCTAGA

6799   CCATCAAGGTGCCTGGGACTGGGGAGGGGCCGGTGCTTCCCAGGTCTGTCTTCACTGGGT
       CCTCCCAGCAGCACTGGGGGCTGGGCACAGCTGTCCTCATTTGATAGATATGGAAATGGA
       GGCTCAGAGGGGTTAAGTGCTTTTCTCAGTTTGCACAATGGCAACAGCAGAGTGGGGGCT
       CACAGGTCGTCAGGGACCCCAAAGCTAGTACTTTTTTTTTTTTTTTTAAGACAGGGTCTC
       TCTCTCTGTTGTCCAGACTGGAGTTCAGTGGTGCAGTCACAAGCTCACTGCAGCCTTGAA
       [C,T]
       TCCTGAGCTCAATCGATCCTCCCACCTCAGCCTCCTGAGTAGCTGGGACTACAGGTGTAC
       GCCACCATGCCTAATTTTTGTATTGTTATTAATTTTTTTTTTTTTTTTTAGAGATGGGG
       TTTTGCCATGTTGCCCAGACTGGTCTTGAACTCCTGGGCTCAAGTGATCCGCCTGCCTTG
       GCCTCCCAAAGTGCTGAGATTATGGCTTGAGCCATTGTGCCTTGCCACTTGTAGTTTCTT
       CTTTTCTTTCTCCTTCATTTTTTATTATTTTTGAAGTATTTTGAAGTATTGAGTAACATA

9579   CTGGTTGGGGCTGTGGACTGAGGTCTGATCTCCAGGCTGGTATGTGGACTGTGGGCAGTT
       TGAACTGGGCTGGGTCCCGGGTTGAGTTCTGGCAATGGGCTGTGTTCTAGGGCTGGGCC
       AAGCTCTGCATTCTGTGGGCAGGGGTGGTTTCTAAGCATGGCCCTGGGCTCGGAGTGAAG
       TTCTGGGCTTGGCTTTACACTTGGTCTTGGGGTCTAGGGTGGGAGTTGGGTTCTGGTTTA
       GATCCAGACAAGGTTCTAGACATTGGGCTGGGGCTTAAGTGTTAAGGTTTGGAGTGGATT
       [C,A]
       TTAGCTGCTTCTGGGCTCTGGAGGGGATCAGGGTTGAAATCAGAGCTTCTGGCTGGGTTC
       CGACCTGGCTTCTTCCCTGACATCTTGGCAATATGTTGTGTTCAAGGTTTGGGGCCATGC
       TGTGGTTTGATCTGTGCGCTGGGATGACATGGGGGTTGCTGTGCTGTGTTCTAAGCCAGG
       CTTTGTCCTGAGTCTAGCTTCTGACCCGAGCTCTGGCTGAGCTGTGGCCTCTAGGTCGAC
       CTTTGGCCCTGGGCTCTGTGGCCGTGGGCAGGGGCCAGTGGGGGTGATCAGATCTGTGTG

9842   TGGGCTGGGGCTTAAGTGTTAAGGTTTGGAGTGGATTCTTAGCTGCTTCTGGGCTCTGGA
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FIGURE 3J

GGGGATCAGGGTTGAAATCAGAGCTTCTGGCTGGGTTCCGACCTGGCTTCTTCCCTGACA
TCTTGGCAATATGTTGTGTTCAAGGTTTGGGGCCATGCTGTGGTTTGATCGTGCGCTGG
GATGACATGGGGGTTGCTGTGCTGTGTTCTAAGCCAGGCTTTGTCCTGAGTCTAGCTTCT
GACCCGAGCTCTGGCTGAGCTGTGGCCTCTAGGTCGACCTTTGGCCCTGGGCTCTGTGGC
[T,C]
GTGGGCAGGGGCCAGTGGGGGTGATCAGATCTGTGTGTCCCAGGTGTCTCTGGATCAGTA
TCAGACGGAGGATGAGCTGTACCAGCTGTCCCTGCAGCGGGAGCCGCGCTCCAAGTCCTC
GGTGAGGGGGTACTCCCTCCTCTCCACTCTGCCCTTCCCTCCTGAGAATCCCAGGATGTG
AGGATGGGAAGAGCTCTTAGCAGCCACCTCACCCATCCATCTTGTAGGACAGAGGCATCC
TGGGGGTAGGGCAGTAGTGTTGGGCAGACTTCCCTCTCCCAGGGATTCCCCTCTCTGTTC

10159   GGGGGTGATCAGATCTGTGTGTCCCAGGTGTCTCTGGATCAGTATCAGACGGAGGATGAG
        CTGTACCAGCTGTCCCTGCAGCGGGAGCCGCGCTCCAAGTCCTCGGTGAGGGGGTACTCC
        CTCCTCTCCACTCTGCCCTTCCCTCCTGAGAATCCCAGGATGTGAGGATGGGAAGAGCTC
        TTAGCAGCCACCTCACCCATCCATCTTGTAGGACAGAGGCATCCTGGGGGTAGGGCAGTA
        GTGTTGGGCAGACTTCCCTCTCCCAGGGATTCCCCTCTCTGTTCCCCGGGGCTCTGGGCT
        [T,C]
        CCCCTGCCTCTGGCCCTAGCTCAGGCCCGACCATTTCCATAGCCAACCAGCCCCACGAGT
        TGCACCCCACCACCCCGGCCCCCGGTACTGGAGGAGTGGACCTCGGCTGCCAAACCCAAG
        CTGGATCAGGCCCTCGTGGTGGAGCACATCGAGAAGATGGTGGAGGTGAGCTCCTGCGGA
        GCCTGAGCAGTGTGTGGGGAGAGGCCAGTTTGCCGGAGCACTGCCCTGGAAGCCAGCACG
        AGTGTCCTGTTCAAGACCCAGCACTCAGCCCCTAGGAGTCACAGGGCCTGGCAGGCCAGC

12025   TGGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACTCTTGACCTCAAGTGATCTACCTG
        CCTTGGCCCCCCAAAGTGCTAGGATTACAGGCATGAGCTACTGCTCCTAGCCTAAAAAAA
        TTTTTTTTGGGCATGGGTGGCACGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAG
        GAGGAACCCTTGAGCCCAGGAGGTTGAGACTGCAGTGAGCTGTCATCACACCACTGCACT
        TCAGCCTGGGTGACTGCGCGAGATCACCCCCATCAAAAAAAAAAAAAAAAAAGAAAAAAAAA
        [A,-,G]
        GAAGAAATGAAAGTCCCCTCTTTCCTTTTCCACTGGTAGAAGTTGCCATGATTAAGCACT
        GTTAACAATATTAAGCTTGGCAGTATGTGGATTCTTCCAGTCTTCTTTTCCCAGGCAGGT
        GCACATTGATAGAGATTTTGTTTGTTTGGTGTCTGTTTCATGGACAAACAGGATTAGAGC
        ATAAATCTAGTTCTGCTTGTGGCTTTTATCATAGCTGCTTTATTTCTTCTCCCAGATTTT
        AGGCAGAGGTAGTTGAGTTCCATGTTTTCTCCCTGGGTTGGTGGGTGGATTTTTATCTAG

14723   GGCTTCTGGGATTTGTGTTCGGGGTAGAAAGGCCCTCAGCCCCTCAAGATTATAAAATTA
        TAAAACCTTTTCTTTTTTTTTTTTTTTTCTGAGACAGGGTGTCTTGCCATGTCACCCAGG
        CTGGAGTGCAGTGGCATGATCTTGGCTCGCTGCAACCTCCACCTCCCAGGTTCAAGTGAT
        TCTCGTGCCTTAGCCTCCCGAGTAGCTGGGATTATAGGTGCCTGCCACTATGCCTGGCTA
        ATTTTTTGTATTTTTAGTAGAGACGGGGCTTTGCCATGTTGGCCAGGCTGGTCTTGAACT
        [T,C]
        CTGACCTCGTGATCCACCCGCCTTGGCCTCCCAAAGTGCTGGGACTACAGGCGTAAGCCA
        CTGTGCTCGGCCCTATATTTTTTTCAGATAGCCAGTTATCCTAATGCTCCCTTGATTTGA
        TGGACCACCTGGATCACACATTATGAGCCCCCTCATAAGCAGGTGGGAGTCTCAAGCGAG
        GGCCAGTCCCGATGGGAATAGCACTTGGTGGCTGAGGACCCTCCTATCTGTGCAGACACT
        GTTGTAAAACTTCACATGCATCATCTAATTTAGTCCTCACCAAAATCCTATGAAATGTAG

14996   CCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCGTGATCCACCCGCCTTGGCCTCCC
        AAAGTGCTGGGACTACAGGCGTAAGCCACTGTGCTCGGCCCTATATTTTTTTCAGATAGC
        CAGTTATCCTAATGCTCCCTTGATTTGATGGACCACCTGGATCACACATTATGAGCCCCC
        TCATAAGCAGGTGGGAGTCTCAAGCGAGGGCCAGTCCCGATGGGAATAGCACTTGGTGGC
        TGAGGACCCTCCTATCTGTGCAGACACTGTTGTAAAACTTCACATGCATCATCTAATTTA
        [G,A]
        TCCTCACCAAAATCCTATGAAATGTAGGAATGATCATTACACCCATTTATAGATAAGGAA
        ACGGAGGGACAGGGAGATTACTCCGCTACAGGTCAAGAGGCAGGGAAGTAGAGCTGCGAT
        TTGAACTGAGGTCTGTGTCTAGAACACGTGCTCATTCTTTCCCTAAAATGTATTCATAGG

FIGURE 3K

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        TGAAAAAGGGCTTCTGCGGAAAGCCCTGGGTTATGTGGGAAACCCTGGATTTACAGCTGT
        CTTTCCAGCAGGATGATGCAGGAGAGAGAGGGATGCGATTTCTCCCAATCTCTCCTGGTC

16153   CGCCCCTCCAGCCCCGGCCCCGCCCTCCCTTCTGGCCCCGCCTCTGCCAGAGCCCTTCTC
        AAGCCAGGAAAACCTGGTAATTCTATTTGCCTCTCCTCCTGTGGTTCTGCCCGGGGCCCT
        GAGGCGGGCTCTAAAGCCCTAGTCTCACCCTCAAGAAGGAAGAAGTAGAGTCATCACCTC
        TAAATCCCTCCTCCCACCACGGCCCCTCCTCTATTGCAGATCCTGGGCATCTACAAGCAG
        GGCCTCAAATGCCGAGGTGAGATGGAATGACTGGAAGGGCTGCTGGGCAGTGTTTTTTTT
        [T,G]
        TTTGTTTGTTTGTTTGGGAGAGTTACTATTTTGGTGGGGCAATTGCCAAGGAGTGAAGTA
        CCTTAAAATCAGAGGCGCATGGCCGGGCATGGTGGCTCAAGCCTGTAATCCCAGCACTTT
        GGGAGGCCGAGGCGCGCAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGACCAACAT
        AGCGCAACCCCGCCTCTACTAAAAATACAAAAAGTAGCTGGGCGTGGTGGCACCCACCTG
        TAATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCGCTTGAACCTGGGAGGCGGGGTT

16181   CTTCTGGCCCCGCCTCTGCCAGAGCCCTTCTCAAGCCAGGAAAACCTGGTAATTCTATTT
        GCCTCTCCTCCTGTGGTTCTGCCCGGGGCCCTGAGGCGGGCTCTAAAGCCCTAGTCTCAC
        CCTCAAGAAGGAAGAAGTAGAGTCATCACCTCTAAATCCCTCCTCCCACCACGGCCCCTC
        CTCTATTGCAGATCCTGGGCATCTACAAGCAGGGCCTCAAATGCCGAGGTGAGATGGAAT
        GACTGGAAGGGCTGCTGGGCAGTGTTTTTTTTGTTTGTTTGTTTGTTTGGGAGAGTTACT
        [G,A]
        TTTTGGTGGGGCAATTGCCAAGGAGTGAAGTACCTTAAAATCAGAGGCGCATGGCCGGGC
        ATGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGCGCAGATCACCTGA
        GGTCAGGAGTTCAAGACCAGCCTGACCAACATAGCGCAACCCCGCCTCTACTAAAAATAC
        AAAAAGTAGCTGGGCGTGGTGGCACCCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGC
        ATGAGAATCGCTTGAACCTGGGAGGCGGGGTTTGCAGTGAGCCGAGATCACGCCACTGCA

16756   CAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGCAACAGAGAGGGCTCTGTCTCA
        AAAAAAAAAAACAACAAAAAAACCCCCAAAACCAAAACCCCACAAAATCAGAGGCTCAAG
        ATGACTGATGTGAAGGGAGTGGCGTTTAAGAGGCCATTTATTTTGATGACGCAGCTGCCC
        AGGAACAGAGAACATGGGAGAAGGCATAGACTGACAATTAGGAGGAGGAGAACACTTTGG
        AAGGAGACTCTTATTTTGGTGGGGCAGCTGCTCAGGAACAAAGGTTCCTGGTAGGGGGGC
        [A,G]
        CAAGCCTGCGGGATGGGATGGAGGGTATTCTGACCAATGTCCCTGGCTGGCTCTCCATTT
        GCTCTCCCCCAGCCTGTGGAGTGAACTGCCACAAGCAGTGCAAGGATCGCCTGTCAGTTG
        AGTGTCGGCGCAGGGCCCAGAGTGTGAGCCTGGAGGGGTCTGCACCCTCACCCTCACCCA
        TGCACAGCCACCATCACCGCGCCTTCAGCTTCTCTCTGCCCCGCCCTGGCAGGCGAGGCT
        CCAGGCCTCCAGGTAAGAGGGAGTCATTCTGTACTGGCCTGTGGAGGGAAGGATGCAGGG

18059   AATGATTATTTTGCTGAGAACAGTCCGAACAACTATGTTAAACTGGGGTCTAAGGTAGTT
        GATCACAACTGTTTGGGTTGGCATAAGTCCTCAAAAAACAGAGGCAGGCACAGGGCATAC
        ATCCTCAAAAATAGAAAAGATAAATCCATTTGCATTGAGCCTTCCAGAAGTGCTGGGGTC
        TAAAATGTGAAATACACACAAAATTGACATTTAAGCAAACTGCGCTGACAAATCTGTGGC
        TGAAAAAGCTGTGGCAAAACAAAAACATAGAAAAAGAGCCTCAAAAATTGGGCTGAGGCC
        [A,G]
        GGCATGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAAGCCAAGGTGGGTGGATCACC
        CGAGGTCAGGAGTTGGAGACCAGACTGGCCAACGTGGCAAAACATCATCTCTACAATACA
        AAAATACAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGG
        CTGAGGCACGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGAGAGCCGAGATTGCGC
        CATTGCACTCCAGCCTGGGCGACAGAGAGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAA

18364   TGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAAGCCAAGGTGGGTGGATCACCCGAG
        GTCAGGAGTTGGAGACCAGACTGGCCAACGTGGCAAAACATCATCTCTACAATACAAAAA
        TACAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGA
        GGCACGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGAGAGCCGAGATTGCGCCATT
        GCACTCCAGCCTGGGCGACAGAGAGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 3L

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        [A,-,T]
        TGGGCTGTGAGGTCATGCAGGGAATTGATTTTTGGTGGGTGGGTCTGCTTCTGGGATGAT
        GTGGATGCCTCCCGTGGAGAGGGGAAGGGTTGATGAAGTCCCAGGGACCTGGAAGTGTGT
        TCTGCAGCAATCCCCCTCCCAGCAGAGATCCGTGAGGAGGAGGTACAGACGGTGGAGGAT
        GGGGTGTTTGACATCCACTTGTAATAGATGGTGAGTCCTCCCACAGCTGGCACCAGAGCT
        CCCCACTGAGGGCTGGGGGGGAGCTGGGGAGTATCAGGGAAATGGGTGCTTTATCCAAAT

18861   ACTTGTAATAGATGGTGAGTCCTCCCACAGCTGGCACCAGAGCTCCCCACTGAGGGCTGG
        GGGGGAGCTGGGGAGTATCAGGGAAATGGGTGCTTTATCCAAATGGCTCCAAGCCAGGTG
        GGCTACTACCTTGTTGTTAGGGGGGTGTCTTCCTCACAACCTGTTTTTCTCTTCCCAGCT
        GTGGTTGGATCAAGGACTCATTCCTGCCTTGGAGAAAATACTTCAACCAGAGCAGGGAGC
        CTGGGGGTGTCGGGGCAGGAGGCTGGGGATGGGGGTGGGATATGAGGGTGGCATGCAGCT
        [G,A]
        AGGGCAGGGCCAGGGCTGGTGTCCCTAAGGTTGTACAGACTCTTGTGAATATTTGTATTT
        TCCAGATGGAATAAAAAGGCCCGTGTAATTAACCTTCACCATCAGCGCCTAGAATCCCGG
        GGGGTAGGGGGATGGTATACTTTACAGGATGACAATCTTGGGAGCTAGAACTTTGTAGCC
        AGAGAAACTTGGGAGGTCTGGAATCTCATGTGTCTGGAGTCTTGGGGAAGAGAATCTTAG
        AAGCAGAAAACCTTGGAACATAAGAATCTTGGGGAGGGTCTAGGATCTTGAGGAGACCAG

20443   TGTTGTGAAGAGCAGCTCGCTCCTGTGCCGCCTGCCTCCTGTGCTGCCTCCATCCCTGCA
        GCCCAGTCGGTTCCTCTTGGCTCCTCTCGTCACTACCCTCCAGTTCCAGTCTGGCCTCTT
        CCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGCATGCATGCATATGTGTGTCC
        AGGTCTGCCTGCCCGGGATGTGACAAGTAGCGGTCTTCATGGTTGCATGTGTCTGAATTT
        GGTGTCTGAGCTTCACATTGTATGCGCCTGTGTGCATGTGTGTGCATGGACATGCATGCT
        [G,A]
        TATCTGCTGTGTTTCCCCTCCCCCATGTGTCCCCACTGGCCTTTGCACATGGGAGAAGGG
        CATGTGCTCAGCATATCACTCAACTGTCCACATTGGGTGGGTACCTGTGTGTGGTGTGTG
        TGTGTGGGGGGTGTGTCTTGAAGTGGCAGGTCCCAAATGCTTAGGCAATCTGAACCTTGG
        ACCTTGCAGAGAGGAGAGATGTCCCTGTAGGTGGGAGGGACAGGGAGATGCAGCAGCTGC
        CCGGTGACCTTTTCTGCCCTTGATGGGCAAAGCTGGGGGTAGGGAAAGGAGACAAGTGCT

20881   TTGAAGTGGCAGGTCCCAAATGCTTAGGCAATCTGAACCTTGGACCTTGCAGAGAGGAGA
        GATGTCCCTGTAGGTGGGAGGGACAGGGAGATGCAGCAGCTGCCCGGTGACCTTTTCTGC
        CCTTGATGGGCAAAGCTGGGGGTAGGGAAAGGAGACAAGTGCTCATACTTACCTCCCTCC
        CTGCCCAGGCTCCTCTGTAAGGGTCTGAGTCTGTCTCTGTGAGCCATTGCATCTGTCTGT
        CTATGCCCTGATGCCTGGATGGACAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
        [A,T]
        GTGTGAGGCTGCAGGAAGAGGAACAGTGGGGGATGGGCAGGAAAGTGGGCTGTGGGGTCA
        GGGAGGCGAT
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FIGURE 3M